

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 17:24:39 ; Search time 59 Seconds
(without alignments)
2504.616 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2768	100.0	523	3	AAB24025	Aab24025 Human PRO
2	2768	100.0	523	3	AAY99419	Aay99419 Human PRO
3	2768	100.0	523	4	AAB66168	Aab66168 Protein o
4	2768	100.0	523	6	ABO33661	Abo33661 Novel hum
5	2768	100.0	523	7	ABO44514	Abo44514 Human sec
6	2768	100.0	523	7	ABO33538	Abo33538 Novel hum
7	2768	100.0	523	7	ADC18151	Adc18151 Human PRO
8	2768	100.0	523	7	ADD70797	Add70797 Human sec
9	2768	100.0	523	7	ADD39874	Add39874 Human sec

10	2768	100.0	523	7	ADD70320	Add70320	Human	sec
11	2768	100.0	523	7	ADD38441	Add38441	Human	sec
12	2768	100.0	523	7	ADD39397	Add39397	Human	sec
13	2768	100.0	523	7	ADD38920	Add38920	Human	sec
14	2768	100.0	523	7	ADD40351	Add40351	Human	sec
15	2768	100.0	523	7	ADE50572	Ade50572	Human	sec
16	2768	100.0	523	7	ADE20184	Ade20184	Human	sec
17	2768	100.0	523	7	ADE50095	Ade50095	Human	sec
18	2768	100.0	523	7	ADE21653	Ade21653	Human	sec
19	2754	99.5	523	4	AAB88348	Aab88348	Human	mem
20	2547	92.0	489	5	AAO22789	Aao22789	Protein	o
21	2198	79.4	523	4	AAE02629	Aae02629	Human	sec
22	2198	79.4	523	5	AAE16939	Aae16939	Human	UDP
23	2198	79.4	523	5	ABB80590	Abb80590	Human	sbg
24	2194	79.3	523	5	AAE15435	Aae15435	Human	dru
25	2193	79.2	523	6	ADA55359	Ada55359	Human	pro
26	2191	79.2	523	5	ABG31867	Abg31867	Human	dru
27	1823	65.9	523	4	AAE02630	Aae02630	Mouse	sec
28	1751	63.3	393	5	ABB80589	Abb80589	Human	sbg
29	1294	46.7	526	4	ABG20645	Abg20645	Novel	hum
30	1142	41.3	318	4	ABB12293	Abb12293	Human	PRO
31	963	34.8	221	7	ADB64627	Adb64627	Human	pro
32	716.5	25.9	527	5	ABP71237	Abp71237	Human	326
33	714.5	25.8	527	4	AAU29284	Aau29284	Human	PRO
34	714.5	25.8	527	5	AAU77927	Aau77927	Human	dru
35	714.5	25.8	527	5	AAE15434	Aae15434	Human	dru
36	714.5	25.8	527	6	ABU58660	Abu58660	Human	PRO
37	714.5	25.8	527	6	ABU88208	Abu88208	Novel	hum
38	714.5	25.8	527	6	ABU84523	Abu84523	Human	sec
39	714.5	25.8	527	6	ABR66397	Abr66397	Human	sec
40	714.5	25.8	527	6	ABR65787	Abr65787	Human	sec
41	714.5	25.8	527	6	ABU99727	Abu99727	Human	sec
42	714.5	25.8	527	6	ABU82966	Abu82966	Human	PRO
43	714.5	25.8	527	6	ABU90087	Abu90087	Novel	hum
44	714.5	25.8	527	6	ABR68336	Abr68336	Human	sec
45	714.5	25.8	527	6	ABU96389	Abu96389	Novel	hum

ALIGNMENTS

RESULT 1

AAB24025

ID AAB24025 standard; protein; 523 AA.

XX

AC AAB24025;

XX

DT 25-JAN-2001 (first entry)

XX

DE Human PRO1780 protein sequence SEQ ID NO:13.

XX

KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;

KW identification; tumourigenesis; anticancer; detection.

XX

OS Homo sapiens.

XX

PN WO200053750-A1.

XX
PD 14-SEP-2000.
XX
PF 02-DEC-1999; 99WO-US028551.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX
DR WPI; 2000-594320/56.
DR N-PSDB; AAC58107.
XX
PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO
PT polypeptide activity or expression.
XX
PS Claim 61; Fig 10; 226pp; English.
XX
CC The present invention describes an antibody that binds to a human protein
CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
CC activity and can be used to diagnose tumours in mammals, by detecting
CC complex formation when the antibody is contacted with test cells.
CC Increased expression of genes encoding (I) can also be detected to
CC diagnose tumours. Agents which inhibit the activity of (I), especially
CC the antibodies, or an antisense oligonucleotide which hybridises to genes
CC encoding (I), can be used to inhibit tumour growth, preferably by
CC inducing cell death. Methods from the present invention can be used to
CC identify compounds which inhibit the biological activity of (I). AAC58019
CC to AAC58102 represent PCR primers and hybridisation probes used in
CC examples from the present invention for human PRO sequences. AAC58103 to
CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
CC protein sequences given in the exemplification of the present invention
XX
SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 3; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
|
Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy 61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
|
Db 61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
|

Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSD	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSD	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVP MVGIP LFGDQPENMVRVEAKKFGVSIQLKKL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVP MVGIP LFGDQPENMVRVEAKKFGVSIQLKKL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKP	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKP	480
Qy	481	HEQYLFDFVVFLLGLTLGTLWL CGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVVFLLGLTLGTLWL CGKLLGMAVWWLRGARKVKET	523

RESULT 2

AA Y99419

ID AAY99419 standard; protein; 523 AA.

XX

AC AAY99419;

XX

DT 08-AUG-2000 (first entry)

XX

DE Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.

XX

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;

KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX

OS Homo sapiens.

XX

PN WO200012708-A2.

XX

PD 09-MAR-2000.

XX

PF 01-SEP-1999; 99WO-US020111.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

PR	09-SEP-1998;	98US-0099602P.
PR	09-SEP-1998;	98US-0099642P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099792P.
PR	10-SEP-1998;	98US-0099808P.
PR	10-SEP-1998;	98US-0099812P.
PR	10-SEP-1998;	98US-0099815P.
PR	10-SEP-1998;	98US-0099816P.
PR	15-SEP-1998;	98US-0100385P.
PR	15-SEP-1998;	98US-0100388P.
PR	15-SEP-1998;	98US-0100390P.
PR	16-SEP-1998;	98US-0100584P.
PR	16-SEP-1998;	98US-0100627P.
PR	16-SEP-1998;	98US-0100661P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100710P.
PR	17-SEP-1998;	98US-0100711P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	18-SEP-1998;	98US-0101071P.
PR	22-SEP-1998;	98US-0101279P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101474P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101476P.
PR	23-SEP-1998;	98US-0101477P.
PR	23-SEP-1998;	98US-0101479P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101915P.
PR	24-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.

PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.

XX

PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-237871/20.
 DR N-PSDB; AAA37101.
 XX
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX
 PS Claim 12; Fig 160; 773pp; English.
 XX
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX
 SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 3; Length 523;
 Best Local Similarity 100.0%; Pred. No. 6.3e-278;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Qy	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPVPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPVPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480

Qy 481 HEQYLFDFVFVFLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET 523
 ||||||||||||||||||||||||||||||||||||||||
 Db 481 HEQYLFDFVFVFLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET 523

RESULT 3

AAB66168

ID AAB66168 standard; protein; 523 AA.

XX

AC AAB66168;

XX

DT 02-APR-2001 (first entry)

XX

DE Protein of the invention #80.

XX

KW Secreted; transmembrane; gene therapy.

XX

OS Unidentified.

XX

PN WO200078961-A1.

XX

PD 28-DEC-2000.

XX

PF 18-FEB-2000; 2000WO-US004342.

XX

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI Williams PM, Wood WI;

XX

DR WPI; 2001-071395/08.

XX

PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.

XX

PS Claim 1; Fig 160; 787pp; English.

XX

CC The present invention relates to secreted and transmembrane proteins.

CC These proteins and the DNA encoding them may be used as hybridization

CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy

XX

SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 4; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
        |||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |||
Db     61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPFVAILSTSFGSLEFGLPIP 180
        |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
        |||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
        |||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
        |||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
        |||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480
        |||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
        |||
Db    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
```

RESULT 4

ABO33661

ID ABO33661 standard; protein; 523 AA.

XX

AC ABO33661;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780.

XX

KW Human; secreted and transmembrane protein; PRO; angiogenesis;

KW endothelial cell proliferation; wound healing; immune response;

KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;

KW cardiac insufficiency disorder; calcium flux; inflammation;

KW vascular endothelial growth factor-stimulated proliferation;

KW mammalian kidney mesangial cell proliferation; Berger disease;

KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;

KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;

KW pancreatic beta-cell precursor cell differentiation; thalassemias;

KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;

KW cartilage disorder; sports injury; arthritis.

XX

OS Homo sapiens.

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PN US2003073130-A1.

XX

PD 17-APR-2003.

XX

PF 11-DEC-2001; 2001US-00015869.

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PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

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PR 10-SEP-1998; 98US-0099741P.

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PR 10-SEP-1998; 98US-0099763P.

PR 10-SEP-1998; 98US-0099792P.

PR 10-SEP-1998; 98US-0099808P.

PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98US-0099815P.

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PR 17-SEP-1998; 98US-0100710P.

PR 17-SEP-1998; 98US-0100711P.

PR 17-SEP-1998; 98US-0100919P.

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PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
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PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.
PR	28-OCT-1998;	98US-0106029P.
PR	28-OCT-1998;	98US-0106030P.
PR	28-OCT-1998;	98US-0106032P.

PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
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PR 10-NOV-1998; 98US-0107783P.
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PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

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PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2003-585293/55.

DR N-PSDB; ACD68440.

XX

PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

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Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR 60

Qy 61 GPFMPDFKKEEKSQVISW LAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
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Db 61 GPFMPDFKKEEKSQVISW LAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180
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Qy 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL 240
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Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
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Qy 301 GSMVNTCQNPEIFKEMNNAFAHL PQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
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Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
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RESULT 5

ABO44514

ID ABO44514 standard; protein; 523 AA.

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AC ABO44514;

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DT 01-OCT-2003 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; vulnerary; cardiant;

KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;

KW adrenal cortical capillary; endothelial cell growth; wound healing;

KW stimulated T-lymphocyte proliferation; immune response suppression;

KW neonatal heart hypertrophy; cardiac insufficiency disorder;

KW vascular endothelial growth factor; inflammation; mononuclear cell;

KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;

KW chondrocyte redifferentiation; bone disorder; cartilage disorder;

KW sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2003044841-A1.

XX

PD 06-MAR-2003.

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PF 06-DEC-2001; 2001US-00006856.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

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PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

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PR 10-SEP-1998; 98US-0099741P.

PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.

PR 10-SEP-1998; 98US-0099792P.

PR 10-SEP-1998; 98US-0099808P.

PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98US-0099815P.

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PR	30-DEC-1998;	98US-0114223P.
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PR	16-APR-1999;	99US-0129674P.
PR	23-JUN-1999;	99US-0141037P.
PR	20-JUL-1999;	99US-0144758P.
PR	26-JUL-1999;	99US-0145698P.
PR	01-SEP-1999;	99WO-US020111.
PR	15-SEP-1999;	99WO-US021194.
PR	29-OCT-1999;	99US-0162506P.
PR	30-NOV-1999;	99WO-US028313.
PR	02-DEC-1999;	99WO-US028551.

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Qy	61	GFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRROOHMOSTFDNTIKEHFTGSRPVLSHL	240

Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPW	480
Qy	481	HEQYLFDFVFVFLGLTLGLTLWLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVFVFLGLTLGLTLWLWLCGKLLGMAVWWLRGARKVKET	523

RESULT 6

ABO33538

ID ABO33538 standard; protein; 523 AA.

XX

AC ABO33538;

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DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1780.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;

KW tissue typing; chromosome identification; vaccine.

XX

OS Homo sapiens.

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PN US2003073129-A1.

XX

PD 17-APR-2003.

XX

PF 04-SEP-2001; 2001US-00946374.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

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PR 05-JAN-1999; 99WO-US000106.
PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 18-OCT-1999; 99US-00403297.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
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PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
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PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

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PA (GETH) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

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DR WPI; 2003-585292/55.

DR N-PSDB; ACD68086.

XX

PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.

XX

PS Claim 12; Fig 160; 561pp; English.

XX

CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I), having at least 80% sequence identity to a sequence

Query Match

100.0%; Score 2768; DB 7; Length 523;

Best Local Similarity 100.0%; Pred. No. 6.3e-278;
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RESULT 7

ADC18151

ID ADC18151 standard; protein; 523 AA.

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AC ADC18151;

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DT 18-DEC-2003 (first entry)

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DE Human PRO polypeptide #80.

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KW Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
KW genetic disorder.

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OS Homo sapiens.

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PN US2003064925-A1.

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PD 03-APR-2003.
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PF 10-DEC-2001; 2001US-00013907.
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PR 22-DEC-1998; 98US-0113296P.
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PR 16-APR-1999; 99US-0129674P.
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PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
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PR 15-SEP-1999; 99WO-US021194.
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PR 16-DEC-1999; 99WO-US030095.
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PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

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PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2003-555602/52.
 DR N-PSDB; ADC18150.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 12; SEQ ID NO 282; 555pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The sequences are useful in the preparation of a
 CC medicament for treating a condition responsive to a PRO polypeptide. The
 CC polypeptides are useful in a number of functional biological assays, as
 CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 2768; DB 7; Length 523;
 Best Local Similarity 100.0%; Pred. No. 6.3e-278;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
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Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMOSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMOSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVQDLENFIAKFGDSGFVLVTL	300
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Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW	480
Qy	481	HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523

ADD70797

ID ADD70797 standard; protein; 523 AA.

XX

AC ADD70797;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003099625-A1.

XX

PD 29-MAY-2003.

XX

PF 12-DEC-2001; 2001US-00015386.

XX

PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

PR 09-SEP-1998; 98US-0099602P.

PR 09-SEP-1998; 98US-0099642P.

PR 10-SEP-1998; 98US-0099741P.

PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.

PR 10-SEP-1998; 98US-0099792P.

PR 10-SEP-1998; 98US-0099808P.

PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98US-0099815P.

PR 10-SEP-1998; 98US-0099816P.

PR 15-SEP-1998; 98US-0100385P.

PR 15-SEP-1998; 98US-0100388P.

PR 15-SEP-1998; 98US-0100390P.

PR 16-SEP-1998; 98US-0100584P.

PR 16-SEP-1998; 98US-0100627P.

PR 16-SEP-1998; 98US-0100661P.

PR 16-SEP-1998; 98US-0100662P.

PR 16-SEP-1998; 98US-0100664P.

PR 17-SEP-1998; 98US-0100683P.

PR 17-SEP-1998; 98US-0100684P.

PR 17-SEP-1998; 98US-0100710P.

PR 17-SEP-1998; 98US-0100711P.

PR 17-SEP-1998; 98US-0100919P.

PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	18-SEP-1998;	98US-0101071P.
PR	22-SEP-1998;	98US-0101279P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101474P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101476P.
PR	23-SEP-1998;	98US-0101477P.
PR	23-SEP-1998;	98US-0101479P.
PR	24-SEP-1998;	98US-0101738P.
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PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101915P.
PR	24-SEP-1998;	98US-0101916P.
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PR	29-SEP-1998;	98US-0102330P.
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PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
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PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
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PR	07-OCT-1998;	98US-0103328P.
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PR	08-OCT-1998;	98US-0103678P.
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PR	08-OCT-1998;	98US-0103711P.
PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
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PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.

PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2003-874602/81.

DR N-PSDB; ADD70796.

XX

PT Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.

XX

PS Claim 12; SEQ ID NO 282; 553pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
|
Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
|
Db 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
|
Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy 181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
|
Db 181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQDLENFIAKFGDSGFVLVTL 300
|
Db 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCShwPKDVHLAANVKIVDWLPQSDLLAH 360
|

Db 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
 |||

Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480
 |||

Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480

Qy 481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
 |||

Db 481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 9

ADD39874

ID ADD39874 standard; protein; 523 AA.

XX

AC ADD39874;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003083462-A1.

XX

PD 01-MAY-2003.

XX

PF 10-DEC-2001; 2001US-00013913.

XX

PR 05-JAN-1999; 99WO-US000106.

PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021194.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006884.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2003-755122/71.

DR N-PSDB; ADD39873.

XX

PT New secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.

XX

PS Claim 12; SEQ ID NO 282; 557pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimaeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. Pro is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,

CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence represents a PRO protein of the invention.
XX
SQ Sequence 523 AA;

Query Match 100.0%; Score 2768; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |||
Db     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP 180
        |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMOSTFDNTIKEHFTGSRPVLSHL 240
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Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMOSTFDNTIKEHFTGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
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Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
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Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
        |||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
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Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
        |||
Db    481 HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
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RESULT 10

ADD70320

ID ADD70320 standard; protein; 523 AA.

XX

AC ADD70320;

XX

DT 15-JAN-2004 (first entry)

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DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003054406-A1.
XX
PD 20-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006818.
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PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
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PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.

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PR	23-SEP-1998;	98US-0101476P.
PR	23-SEP-1998;	98US-0101477P.
PR	23-SEP-1998;	98US-0101479P.
PR	24-SEP-1998;	98US-0101738P.
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PR	24-SEP-1998;	98US-0101743P.
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PR	24-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
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PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
PR	07-OCT-1998;	98US-0103315P.
PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103395P.
PR	07-OCT-1998;	98US-0103396P.
PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	08-OCT-1998;	98US-0103711P.
PR	14-OCT-1998;	98US-0104257P.
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PR	20-OCT-1998;	98US-0105000P.
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PR	22-OCT-1998;	98US-0105266P.
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PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.
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PR	29-OCT-1998;	98US-0106384P.
PR	29-OCT-1998;	98US-0108500P.
PR	30-OCT-1998;	98US-0106464P.
PR	03-NOV-1998;	98US-0106856P.

PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
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PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
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PR 18-NOV-1998; 98US-0108849P.
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PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-708344/67.
 DR N-PSDB; ADD70319.
 XX
 PT Novel isolated PRO polypeptide useful for tissue typing, modulating
 PT biological activity of cell, as molecular weight markers in protein
 PT electrophoresis, for treating arthritis, tumor.
 XX
 PS Claim 12; SEQ ID NO 282; 549pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;
 Best Local Similarity 100.0%; Pred. No. 6.3e-278;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Qy	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480

PR	16-SEP-1998;	98US-0100664P.
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PR	17-SEP-1998;	98US-0100710P.
PR	17-SEP-1998;	98US-0100711P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
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PR	07-OCT-1998;	98US-0103328P.
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PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	08-OCT-1998;	98US-0103711P.
PR	14-OCT-1998;	98US-0104257P.
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PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.

PR 27-OCT-1998; 98US-0105807P.
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PR 29-OCT-1998; 98US-0106384P.
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PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
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PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
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PR 17-NOV-1998; 98US-0108787P.
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PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

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PA (GETH) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

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DR WPI; 2003-787000/74.

DR N-PSDB; ADD38440.

XX

PT Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,
PT thalassemias.

XX

PS Claim 12; SEQ ID NO 282; 556pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 100.0%; Score 2768; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
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Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy 61 GPFMPDFKKEEKSQVISWLAPEHDHREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
|
Db 61 GPFMPDFKKEEKSQVISWLAPEHDHREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
|
Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
|
Db 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
 |||
 Db 241 LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360
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Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPVVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
 |||
 Db 361 PSIRLFVTHGGQNSIMEAIQHGVPVVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480
 |||
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480

Qy 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
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 Db 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 12

ADD39397

ID ADD39397 standard; protein; 523 AA.

XX

AC ADD39397;

XX

DT 15-JAN-2004 (first entry)

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DE Human secreted/transmembrane protein PRO1780.

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KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

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PN US2003096954-A1.

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PD 22-MAY-2003.

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PF 07-DEC-2001; 2001US-00011671.

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PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

PR 09-SEP-1998; 98US-0099602P.

PR	09-SEP-1998;	98US-0099642P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099792P.
PR	10-SEP-1998;	98US-0099808P.
PR	10-SEP-1998;	98US-0099812P.
PR	10-SEP-1998;	98US-0099815P.
PR	10-SEP-1998;	98US-0099816P.
PR	15-SEP-1998;	98US-0100385P.
PR	15-SEP-1998;	98US-0100388P.
PR	15-SEP-1998;	98US-0100390P.
PR	16-SEP-1998;	98US-0100584P.
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PR	16-SEP-1998;	98US-0100661P.
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PR	16-SEP-1998;	98US-0100664P.
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PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
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PR	18-SEP-1998;	98US-0101068P.
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PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101474P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101476P.
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PR	07-OCT-1998;	98US-0103315P.

PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103395P.
PR	07-OCT-1998;	98US-0103396P.
PR	07-OCT-1998;	98US-0103401P.
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PR	14-OCT-1998;	98US-0104257P.
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PR	22-OCT-1998;	98US-0105169P.
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PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
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PR	29-OCT-1998;	98US-0106384P.
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PR	17-NOV-1998;	98US-0108775P.
PR	17-NOV-1998;	98US-0108779P.
PR	17-NOV-1998;	98US-0108787P.
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PR	17-NOV-1998;	98US-0108867P.
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PR	18-NOV-1998;	98US-0108850P.
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PR	18-NOV-1998;	98US-0108858P.
PR	18-NOV-1998;	98US-0108904P.
PR	22-DEC-1998;	98US-0113296P.
PR	30-DEC-1998;	98US-0114223P.

PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
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PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
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PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
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PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

XX

DR WPI; 2003-786999/74.

DR N-PSDB; ADD39396.

XX

PT Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.

XX

PS Claim 12; SEQ ID NO 282; 550pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLINVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLINVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
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Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
Qy	481	HEQYLFDFVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET	523
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RESULT 13

ADD38920

ID ADD38920 standard; protein; 523 AA.

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AC ADD38920;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

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PN US2003092061-A1.

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PD 15-MAY-2003.
XX
PF 06-DEC-2001; 2001US-00007194.
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PI Williams PM, Wood WI;

AC ADD40351;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1780.
 XX
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 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003082627-A1.
 XX
 PD 01-MAY-2003.
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 PF 06-DEC-2001; 2001US-00006117.
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PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

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PR    10-NOV-2000; 2000WO-US030873.
PR    01-DEC-2000; 2000WO-US032678.
PR    28-FEB-2001; 2001WO-US006520.
PR    01-MAR-2001; 2001WO-US006666.
PR    01-JUN-2001; 2001WO-US017800.
PR    20-JUN-2001; 2001WO-US019692.
PR    29-JUN-2001; 2001WO-US021066.
PR    09-JUL-2001; 2001WO-US021735.
PR    04-SEP-2001; 2001US-00946374.
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PA (GETH) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers I, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

DR WPI; 2003-755104/71.

PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT insufficiency disorders.

PS Claim 12; SEQ ID NO 282; 550pp; English.

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 2768; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.3e-278;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      481 HEQYLFDFVFVLLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET 523

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RESULT 15

ADE50572

ID ADE50572 standard; protein; 523 AA.

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AC ADE50572;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1780.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003069179-A1.

XX

PD 10-APR-2003.

XX

PF 11-DEC-2001; 2001US-00015393.

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PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

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PR 02-SEP-1998; 98US-0098803P.

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PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98US-0099815P.

PR 10-SEP-1998; 98US-0099816P.

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PR	30-DEC-1998;	98US-0114223P.
PR	05-JAN-1999;	99WO-US000106.
PR	16-APR-1999;	99US-0129674P.
PR	23-JUN-1999;	99US-0141037P.
PR	20-JUL-1999;	99US-0144758P.
PR	26-JUL-1999;	99US-0145698P.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	674	24.3	533	5	PCT-US92-00282-3	Sequence 3, Appli
2	661.5	23.9	528	4	US-09-356-806-8	Sequence 8, Appli
3	658	23.8	531	5	PCT-US92-00282-6	Sequence 6, Appli
4	657	23.7	530	3	US-09-180-852-2	Sequence 2, Appli
5	651.5	23.5	524	4	US-09-356-806-40	Sequence 40, Appl
6	649	23.4	530	4	US-09-356-806-113	Sequence 113, App
7	629	22.7	531	5	PCT-US92-00282-5	Sequence 5, Appli
8	606	21.9	534	5	PCT-US92-00282-4	Sequence 4, Appli
9	600	21.7	529	5	PCT-US92-00282-7	Sequence 7, Appli
10	521	18.8	454	4	US-09-813-918-2	Sequence 2, Appli
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13	346.5	12.5	515	3	US-08-942-012B-32	Sequence 32, Appl
14	342.5	12.4	460	3	US-08-942-012B-33	Sequence 33, Appl
15	321	11.6	515	3	US-08-942-012B-24	Sequence 24, Appl
16	316.5	11.4	488	3	US-08-942-012B-29	Sequence 29, Appl
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19	300	10.8	288	5	PCT-US92-00282-19	Sequence 19, Appl
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21	259.5	9.4	489	3	US-08-942-012B-31	Sequence 31, Appl
22	258.5	9.3	287	4	US-09-305-856B-10	Sequence 10, Appl
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27	248	9.0	506	3	US-08-942-012B-26	Sequence 26, Appl
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32	242	8.7	491	3	US-08-942-012B-27	Sequence 27, Appl
33	239	8.6	129	4	US-09-370-838-36	Sequence 36, Appl
34	227	8.2	317	4	US-09-305-856B-12	Sequence 12, Appl
35	226	8.2	289	4	US-09-305-856B-6	Sequence 6, Appli
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37	223	8.1	253	4	US-09-305-856B-16	Sequence 16, Appl
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45	175	6.3	56	2	US-08-466-583-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

PCT-US92-00282-3

; Sequence 3, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/00282
;   FILING DATE:  19920110
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  SCOTT, WATSON T.
;   REGISTRATION NUMBER:  26581
;   REFERENCE/DOCKET NUMBER:  91532-PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  202-861-3000
;   TELEFAX:  202-822-0944
;   TELEX:  6714627 CUSH
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  533 amino acids
;   TYPE:  AMINO ACID
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
PCT-US92-00282-3

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Query Match          24.3%;  Score 674;  DB 5;  Length 533;
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Matches 175;  Conservative 92;  Mismatches 212;  Indels 38;  Gaps 13;

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Db      412 TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGA 471

Qy      469 THLKPYVFQQPWHEQYLFDFVFVLLGLTLGLTLWLCGK 505
      ||:| |:: : || ||| : | :: |
Db      472 PHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 508

```

RESULT 2

```

US-09-356-806-8
; Sequence 8, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)
and
; TITLE OF INVENTION: 2B15 (UGT2B15) Genes
; FILE REFERENCE: SEQ-22PRV2
; CURRENT APPLICATION NUMBER: US/09/356,806
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 528
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-356-806-8

```

```

Query Match          23.9%; Score 661.5; DB 4; Length 528;
Best Local Similarity 34.2%; Pred. No. 1.3e-61;
Matches 173; Conservative 87; Mismatches 215; Indels 31; Gaps 15;

```

```

Qy      34 SHYLIMDRVSQILQDHGHNVTMLNHKRG----PFMPDFKKEEKSYQVISWLAPEDHQREF 89
      ||:: : : | || ||:| | | | : : || ::
Db      34 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSPSTLKFVYVPVSLTKTEFEDIKQL 93

Qy      90 KKSFDFFLEETLGGRGKFENLLNVL----EYLAQCASHFLNRKDIMDSLKNENFDMVIVE 145
      | : ::| | : :: : | | :: | : | | : | : :
Db      94 VKRWAELPKDTEFW--SYFSQVQEIMWTFNDILRKFCCKDIVSNKKLMKKLQESRFDVVVLAD 151

Qy      146 TFDYCPF--LIAEKLGPFPVAILSTSFG--SLE---FGLPIPLSYVPVFRSLTLDHMDFWG 199
      || |::| | || | | | ::| || | |||| | | : | |
Db      152 A--VFPFGELLAELLKIPFVYSLRFSPGYAIEKHSGGLLFPPSYVPVVMSELSDQMTFIE 209

Qy      200 RVKN--FLMFFSFCRRQOHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDF 257
      |||| ::::| | : | : : | | | : ||:| | : : | |
Db      210 RVKNMIYVLYFEFWFQIFDMKK--WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 266

Qy      258 ARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM 316
      ||||| :||| || ||:::| | : |::| | : :||| || : | :
Db      267 PHPLLNPVFEFVGGLHCKPAKPLPKEMEETFQSSGENGVVVFSLGSMVSNSTSE--ERANVI 324

Qy      317 NNAFAHLPOGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLFVTHGGQNSIM 376

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      :| | :|| |:| : | | | :| :||:|||| | | | |:|||| | |
Db      325 ASALAKIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTRAFITHGGANGIY 381

Qy      377 EAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
      ||| ||:||||:|||| |||:|: :|| | | : : | :| :| | |
Db      382 EAIYHGIPMVGVPPLFADQPDNIAHMKAKGAAVSLDFHTMSSTDLLNALKTVINDPLYKEN 441

Qy      437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLT 496
      |: | | |: | | | |: |: | | |: | : : | | |||
Db      442 AMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHDLTWFAQYHSLDVTGFLACV 501

Qy      497 LGTLWLCGKLLGMAVW-WLRGARKVK 521
      ::: | | || :| :| |
Db      502 ATVIFIITKCL-FCVWKEFVRTGKKGK 526

```

RESULT 3

PCT-US92-00282-6

```

; Sequence 6, Application PC/TUS9200282
; GENERAL INFORMATION:
;   APPLICANT: OWENS, IDA S.
;   APPLICANT: RITTER, JOSEPH K.
;   TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
;   TITLE OF INVENTION: THEREIN.
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CUSHMAN DARBY & CUSHMAN
;     STREET: 1615 L STREET, N.W.
;     CITY: WASHINGTON
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20036-5601
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/00282
;   FILING DATE: 19920110
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: SCOTT, WATSON T.
;   REGISTRATION NUMBER: 26581
;   REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-861-3000
;   TELEFAX: 202-822-0944
;   TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 531 amino acids
;     TYPE: AMINO ACID
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US92-00282-6

```


Query Match 23.8%; Score 658; DB 5; Length 531;
Best Local Similarity 30.9%; Pred. No. 3e-61;
Matches 171; Conservative 106; Mismatches 211; Indels 66; Gaps 17;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
      : |   |||:   ||   :|  |:| :  : |||:| |  | :|   ||   :|
Db      7 LRGLSGLLLLLLALP---WAEKGKVL-VFPMEGSHWLSMRDVVRELHARGHQAVVL---- 58

Qy     61 GPFMPDFKKEEKSYQVISWLAP---EDHQREF---KKSFD-----FFLEETLGGRGK 106
      | :   | |  : : :: |   |::|||   || |:   ||  ||:   |
Db     59 APEVTVMHKGEDFFTLQTYAFPTYKKEYQREILGNACKGFEPQHFVKTF--ETMASIKK 116

Qy    107 FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPFVAIL 166
      | :|   |   | :  |: | :: | : |||: :   |  |:|: |  | | |
Db    117 FFDL-----YANSCAALLHNKTLIQQLNSSSFVDVLTDPVFPCGALLAKYLQIPAVFFL 170

Qy    167 STSFGSLEF---GLPIPLSYVPVFRSLLTDHMFDFWGRVKNFLMFFS---FCRRQQHMQST 220
      :   :::   | | ||:|   ::|:| | |  ||| |  :   |   |: |
Db    171 RSVPCGIDYEATQCPKPSSYIPNLLTMLSDHMTFLQRVKNMLYPLTLKYIC---HLSIT 226

Qy    221 FDNTIKEHFTEGSR---PVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIK 277
      ::   :   ||| |   | :|   ||-||: ||::|| |:| |:   |
Db    227 PYESLASELLQREMSLVEVLSH----ASVWLFRGDFVFDYPRPIMPNMVFIGGINCVIKK 282

Qy    278 PVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShWP 337
      |: |: | ::   | : | |: :||| |:   :   | : |   :|| ::| :
Db    283 PLSQEFAYVNASGEHGIVVFSLSGSMVSEIPEKKAM-EIAEALGRIPQTLWRYTGT--- 338

Qy    338 KDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPEN 397
      :  :|| |  :| |||:| | |  | |:| | : | | | :||| | :||| | :|
Db    339 RPSNLAKNTILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMMPLFGDQMDN 398

Qy    398 MVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVG 457
      |:| :  |::: : :: | : |   :| :: :| ||   :   | : :   |: |   |
Db    399 AKRMETRGAGVTNLVLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAVF 458

Qy    458 WIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLLGLTLGLTLWL-----CGKLLGM 509
      |::|:: || ||:|   |:: :  ||  ||| : |  ::   | | |
Db    459 WVEYVMRHKGAPHLRPAHDLTWYQYHSLDVGFLLAIVLTVVFIVYKSCAYGCRKCFG- 517

Qy    510 AVWWLRGARKVKET 523
      |  :||:
Db    518 -----GKGRVKKS 525
```

RESULT 4

US-09-180-852-2

; Sequence 2, Application US/09180852

; Patent No. 6287834

; GENERAL INFORMATION:

; APPLICANT: BELANGER, Alain

; APPLICANT: HUM, Dean W.

; APPLICANT: BEAULIEU, Martin

; APPLICANT: LEVESQUE, Eric

; TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE

; TITLE OF INVENTION: DIPHOSPHO-GLUCURONOSYLTRANSFERASE

```
; FILE REFERENCE: 1259-449
; CURRENT APPLICATION NUMBER: US/09/180,852
; CURRENT FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: PCT/CA97/00328
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: US 08/649,319
; EARLIER FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-852-2
```

```
Query Match          23.7%; Score 657; DB 3; Length 530;
Best Local Similarity 32.6%; Pred. No. 3.9e-61;
Matches 159; Conservative 92; Mismatches 211; Indels 26; Gaps 11;
```

```
Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVI-SWLAPEDHQREFKKS 92
      ||:: | : : | || | : | : | : | : | : |
Db      34 SHWINMKTILEELVQRGHEVIVLTSSASILVNASKSSAIKLEVYPTSLTKNDLEDFFMKM 93

Qy      93 FDFLEETLGGRGKFENLLNVLEYLALQCSHF-----LNRKDIMDSLKNENFDMVI 143
      || : : | : : | : | : | : | : | : | : | : | : |
Db      94 FDRWTYSI--SKNTFWSYFSQLQELCWEYSYDYNIKLCEDAVLNKK-LMRKLQESKFDVLL 150

Qy     144 VETFDYCPFLIAEKLKGPFFVAILSTSFSG-SLE---FGLPIPLSYVPVFRSLTDMDFWG 199
      : : | |::| | ||: | | |::| | | | | | | | | | |
Db     151 ADAVNPCGELLAELLNIPFLYSLRFSVGYTVEKNGGGFLFPPSYVPVVMSELSQMI FME 210

Qy     200 RVKN--FLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDF 257
      |::| ::::| | : :: :| | | | | : | | |::| | : : |::|
Db     211 RIKNMIYMLYDFDFWQAYDLKK-WDQFYSE--VLGRPTTLFETMGKAEMWLIRTYWDFEF 267

Qy     258 ARPLLNPNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMN 317
      || ||| :||| | ||:|:::| | : |::| | : :|||:: : | :
Db     268 PRPFLPNVDFVGGLHCKPAKPLPKEMEEFVQSSGENGIVVFSLGSMISN-MSEESANMIA 326

Qy     318 NAFALPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIME 377
      : | | :|| |::| | | | | | | | | | | | | | | | |
Db     327 SALAQIPQKVLWREFD---GKKPNTLGSNTRLYKWLPQNDLLGHPKTKAFITHGGTNGIYE 383

Qy     378 AIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAA 437
      || ||:||||||| || :|: ::|| :|: :: : : | : : : | ||
Db     384 AIYHGIPMVGIPLEADQHDNIAHMKAKGAALSVDIRTMSRDLLNALKSVINDPIYKENI 443

Qy     438 VAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKPYVFQQPWHEQYLFDFVFLGLTL 497
      : | | | : | | ||: |:: || ||: | : : || ||
Db     444 MKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHNLTWIIQYHSLDVIAFLLACVA 503

Qy     498 GTLWLCGK 505
      ::: |
Db     504 TMIFMITK 511
```

RESULT 5

US-09-356-806-40
; Sequence 40, Application US/09356806
; Patent No. 6586175
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; APPLICANT: Miller, Andrew
; APPLICANT: Reidy, Michael
; TITLE OF INVENTION: Genotyping Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)
and
; TITLE OF INVENTION: 2B15 (UGT2B15) Genes
; FILE REFERENCE: SEQ-22PRV2
; CURRENT APPLICATION NUMBER: US/09/356,806
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 524
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-356-806-40

Query Match 23.5%; Score 651.5; DB 4; Length 524;
Best Local Similarity 31.5%; Pred. No. 1.5e-60;
Matches 163; Conservative 87; Mismatches 212; Indels 55; Gaps 14;

Qy	34	SHYLLMDRVSQILQDHGHNVMTLNHKGKRG-PFMPD-----FKKEEKSQY---Q	75
		: : : : : : :	
Db	34	SHWMNIKTILDELIQRGHEVTVLASSASILFDPNNSSALKIEIYPTSLTKTELENFIMQQ	93
Qy	76	VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ-CSHFLNRKDIMDS	133
		: : : : : : : : : :	
Db	94	IKRWSDLPKD-----TFWLYFSQV-----QEIMSIFGDITRKFCKDVVSNNKFKMCK	139
Qy	134	LKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTS----FGSLEFGLPIPLSYVPVFRS	189
		: : : : : :	
Db	140	VQESRFDVIFADAI FPCSELLAELFNIPFVYLSFSFGYTFEKHSGGFIFPPSYVPVMS	199
Qy	190	LLTDHMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTE---GSRPVLSHLLKA	244
		: : : : :	
Db	200	ELTDQMTFMERVKNMIYVLYFDF-----WFEIFDMKKWDQFYSEVLGRPTTLSETMGKA	253
Qy	245	ELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV	304
		: : : : : : : : :	
Db	254	DVWLIRNSWNFQFPYPLLPNVDFVGGLHCKPAKPLPKEMEDFVQSSGENGVVVFSLGSMV	313
Qy	305	NTCQNPEIFKEMNNAFAHLPGQVWKQCQSHWPKDVHLLAANVKIVDWLPQSDLLAHPSIR	364
		: : : : : : : : :	
Db	314	SN-MTEERANVIASALAIQIPQKVLWRFN---KPDTLGLNTRLYKWIPQNDLLGHPKTR	369
Qy	365	LFVTHGGQNSIMEAIQHGVPVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM	424
		: : : : : : : :	
Db	370	AFITHGGANGIYEAIYHGIPVGIPLFADQPDNIAHMKARGAAVRVDFNTMSSTDLLNAL	429
Qy	425	KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQY	484
		: : : : : : : : : : :	

Db 430 KRVINDPSYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAADLTWFQYH 489

Qy 485 LFDVFVFLGLTLGTLWLWLCGKLLGMAVWWLRGARKVK 521
 || ||| ::: | | : ||| |

Db 490 SLDVIGFLLVCVATVIFIVTKCCLFCFW--KFARKAK 524

RESULT 6

US-09-356-806-113
 ; Sequence 113, Application US/09356806
 ; Patent No. 6586175
 ; GENERAL INFORMATION:
 ; APPLICANT: Penny, Laura
 ; APPLICANT: Galvin, Margaret
 ; APPLICANT: Miller, Andrew
 ; APPLICANT: Reidy, Michael
 ; TITLE OF INVENTION: Genotyping Human
 ; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)
 and
 ; TITLE OF INVENTION: 2B15 (UGT2B15) Genes
 ; FILE REFERENCE: SEQ-22PRV2
 ; CURRENT APPLICATION NUMBER: US/09/356,806
 ; CURRENT FILING DATE: 1999-07-20
 ; NUMBER OF SEQ ID NOS: 164
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 113
 ; LENGTH: 530
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 US-09-356-806-113

Query Match 23.4%; Score 649; DB 4; Length 530;
 Best Local Similarity 31.8%; Pred. No. 2.8e-60;
 Matches 155; Conservative 90; Mismatches 218; Indels 24; Gaps 10;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVI-SWLAPEDHQREFKKS 92
 ||:: | : : | || ||: | : | : | | : |

Db 34 SHWINMKTILEELVQRGHEVTVLTSASTLVNASKSSAIKLEVYPTSLTKNDLEDSDLKI 93

Qy 93 FDFEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMVIV 144
 | :: : | : : | : | : | : | : | : | : |

Db 94 LDRWIYGV--SKNTFWSYFSQLQELCWEYYDYSNKLCKDAVLNKKLMMKLQESKFDVILA 151

Qy 145 ETFDYCPFLIAEKLKGPVAILSTSFG-SLE---FGLPIPLSYVPVFRSLTLDHMDFWGR 200
 : : | | : || ||: | | : | | | | | | | | | |

Db 152 DALNPCGELLAELENIPFLYSLRFSVGYTFEKNGGGFLFPPSYVPVVMSELSDQMIFMER 211

Qy 201 VKNF--LMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAEWFINSDFAFDFA 258
 : || : :: | | : : : | | | : | | : | | : |

Db 212 IKNMIHMLYFDFWFQIYDLKK-WDQFYSE--VLGRPTTLFETMGKAEMWLIRTYWDFEFP 268

Qy 259 RPLLNTVYVGGLEMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN 318
 || ||| : |||| || ||: | : : | : | : | : | : | : |

Db 269 RPFLPNVDFVGGLHCKPAKPLPKEMEEFVQSSGENGIVVFSLGSMISN-MSEESANMIAS 327

Qy 319 AFAHLPQGVIVKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEA 378
 | | : || | : : | | : | : : ||| : || | : | : || | | |

Db 328 ALAQIPQKVLWRFD---GKKPNTLGSNTRLYKWLPQNDLLGHPKTKAFITHGGTNGIYEA 384

Qy 379 IQHGVPVVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAV 438
| | : | | | | | | | | | : | : : : | : | : | | :

Db 385 IYHGIPVVGIPLFADQHDNIAHMKAKGAALSVDIRTMSSRDLLNALKSVINDPVYKENVM 444

Qy 439 AASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLLGLTLG 498
| | : | | | | : | : | | | : | : : | | | |

Db 445 KLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWIIQYHSLDVIAFLLACVAT 504

Qy 499 TLWLCKG 505
: : : |

Db 505 VIFIITK 511

RESULT 7

PCT-US92-00282-5

; Sequence 5, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26581

; REFERENCE/DOCKET NUMBER: 91532-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 531 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US92-00282-5

Query Match 22.7%; Score 629; DB 5; Length 531;
 Best Local Similarity 30.4%; Pred. No. 3.8e-58;
 Matches 159; Conservative 100; Mismatches 218; Indels 46; Gaps 13;

```

Qy      4 QRVLLLVGFL-LPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 62
      ||:  | || | |:::  :  |:| :  |||:| | : ::| | || : ::
Db      9 QRISAGVFFLALWGMVVG D--KLLVVPQ-DGSHWLSMKDIVEVLSDRGHEIVVV----- 59

Qy     63 EMPDFK---KEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRG-----KFENLLN 112
      :|:  || | | :  | | | | :  |  |  : :: | :
Db     60 -VPEVNLLLKEYKYYTRKIYPVPYD-QEELKNRYQSEFGNNHFAERSFLTAPQTEYRNNMI 117

Qy    113 VLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFAILSTSFGS 172
      |:  : | | : | ::  |  || :  |  : ::|| || | | :  |
Db    118 VIGLYFINCQSLQDRDTLNNFFKESKFDAFTDPALPCGVILA EYLG LPSVYLFRGFPCS 177

Qy    173 LEFGL---PIPLSYVPVFRSLLTDHMDFWGRVKNFL-----MFFSFCRRQQHMQSTFD 222
      ||  | |::| :  : || | | || ||  :|:  : : : |
Db    178 LEHTFSRSPDPVSYIPRCYTKFSDHMTFSQRVANFLVNLEPYLFYCLFSKYEKLASA-- 235

Qy    223 NTIKEHFTEGSRPVLSHLLKLAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKPVPQD 282
      :|  | |  | :  : | : || : ||::|| |::||:  | | : |:
Db    236 -VLK-----RDVDIITLSEVSVWLLRYDFVLEYPRPVMNMFVIGGINCKKRKDLSEQ 287

Qy    283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCCHWPKDVHL 342
      | :|  | : | | : ||||:  :  : : |  || |::  :  : : |
Db    288 FEAYINASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKNPQTVLWRYTGT---RPSNL 343

Qy    343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLFQDQPENMVRVE 402
      | |  : | |||: || | | |::| | : : | : | : |||| : ||||| : | | : |
Db    344 ANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFGDQMDNAKRME 403

Qy    403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      |  ||:: : : : | |  : | :: || | | :  | : : | : |  | |:: |
Db    404 TKGAGVTINVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFV 463

Qy    463 LQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGLTLWL CGK 505
      ::  || ||:|  |:: :  ||  ||| : |  ::  |
Db    464 MRHKGAPHLRPA AHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 506
  
```

RESULT 8

PCT-US92-00282-4

; Sequence 4, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-00282-4

```

```

Query Match          21.9%; Score 606; DB 5; Length 534;
Best Local Similarity 31.3%; Pred. No. 1.1e-55;
Matches 163; Conservative 94; Mismatches 218; Indels 46; Gaps 13;

```

```

Qy      8 LLVGELLPGVLLS-----EAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 62
      | | || || | : | : | : | | : | | : | | : |
Db     12 LATGLLL---LLSVQPWAESGKVLVVPT-DGSPWLSMREALRELHARGHQAVVLT----P 63

Qy     63 FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLG---GRGKFENLL----- 111
      : | || | : : : | | : | : | | | | : | : |
Db     64 EVNMHIKEEKFFTLTAYAVPWT-QKEFDR-----VTLGYTQGGFFETEHLKRYSRMA 115

Qy    112 ---NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFAVAILST 168
      || | | | : : : | : | : | : | : | : | | |
Db    116 IMNNVSLALHRCCVELLHNEALIRHLNATSFDDVLTDPVNLCGAVLAKYLSIPAVFFWRY 175

Qy    169 SFGSLEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTI 225
      | : | | | | : | : | : | | | | | : : :
Db    176 IPCDLDFKGTQCPNPSSYIPKLLTTNSDHMTFLQRVKNMLYPLALSYICHTFSAPYASIA 235

Qy    226 KEHFTEGSRPV-LSHLLLKAEIWFINSDFAFDFARPLLNTVYVGGLEMEKPIKVPQDLE 284
      | | | | : | : | : | | | : | : | : | : | : |
Db    236 SELF---QREVSVDLVSYASVWLFGRGDFVMDYPRPIMPNMVFIGGINCANGKPLSQEFE 292

Qy    285 NFIAKFGDSGFVLVTILGSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCQSHWPKDVHLAA 344
      : | | : | : : | | : : : | : | : | : : : |
Db    293 AYINASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLAN 348

Qy    345 NVKIVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAK 404
      | : | | | : | | | | : | : | : | : | : | : |
Db    349 NTILVKWLQPNDLLGHMPMtraFiTHAGSHGVYESICNGVPMVMMPLEFGDQMDNAKRMETK 408

```

Qy 405 KFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQ 464
 ||:: : :: :| | :| :: || || : | : : |: | | |:: |::
 Db 409 GAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMR 468
 Qy 465 TGGATHLKPYVFQQPWHEQYLFDFVFVFLGLGLGLWLCGK 505
 || ||:| |:: : || ||| : | :: |
 Db 469 HKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 509

RESULT 9

PCT-US92-00282-7

; Sequence 7, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26581

; REFERENCE/DOCKET NUMBER: 91532-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 529 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US92-00282-7

Query Match 21.7%; Score 600; DB 5; Length 529;

Best Local Similarity 28.3%; Pred. No. 4.8e-55;

Matches 155; Conservative 105; Mismatches 222; Indels 66; Gaps 14;

Qy 8 LLVGFL---LPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHNKRGPFM 64

; TYPE: PRT
; ORGANISM: Human
US-09-813-918-2

Query Match 18.8%; Score 521; DB 4; Length 454;
Best Local Similarity 28.7%; Pred. No. 1e-46;
Matches 128; Conservative 79; Mismatches 173; Indels 66; Gaps 13;

```
Qy      118 ALQCSHFLNRKDIMDSLKNENFDMVIVET-----FDYCPFLIAEKLGKPPFVAILSTSFGS 172
          | : ||::| | | : |      :: : : | |      :
Db      30 AAAYSHWMNMKTILKELVQRGHEVTVLASSASILFD-----PNDAST 71

Qy      173 LEFGLPIPLSYVPV-FRSLTDMDFWGRVK--NFLMFFS-----FCR-- 212
          | : | : | | | : : : | : : | : | : | : | : | :
Db      72 LKFEV-YPTSLTKTEFENIIMQQVKRWSDIRKDSFWLYFSQEQEILWELYDIFRNECKDV 130

Qy      213 -----RQQHMQSTFDNTIKEH-FTEGS-----RP-VLSHLLLKAELWFINSDFAFD 256
          : : : | | : | | | | | | | : | : | : : |
Db      131 VSNKKVMKKLQELRFDIVFADAVFPCGELLAALLNIRPTTLFETMGKADIWLMRNPWSFQ 190

Qy      257 FARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEM 316
          | | ||| : ||| || ||:|::| | : | : | | : : ||| : : | :
Db      191 FPHPFLPNVDFVGGFHCKPAKPLPKEMEETFVQSSGENGVVVFSLGSVISN-MTAERANVI 249

Qy      317 NNAFAHLPQGVIWKCQCSEHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIM 376
          | | : || | : : : | | | : : | : | : | | | | | | | |
Db      250 ATALARIPQKVLWRFDGN---KPDALGLNTRLYKWIPQNDLLGHGPKTRAFITHGGANGIY 306

Qy      377 EAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
          ||| ||:||||||| |||:| : || | : : | : | : : | |
Db      307 EAIYHGIPMVGIPFLFDQPDNIAHMKAKGAARLDENTMSSTDLLNALKTVINDPLYKEN 366

Qy      437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLT 496
          : | | | : | | | | : | | | : | : : | | | |
Db      367 IMKLSRIQHDQPVKPLDRAVFWIEFVMPHKGAKHLRVAADLTWFOYHSLDVIGFLLACV 426

Qy      497 LGTLWLCCGKLLGMAVWWLRGARKVKE 522
          : : : | | | : ||| | :
Db      427 ATVIFIITKFCLECFW--KFARKGKK 450
```

RESULT 11

US-09-813-918-3

; Sequence 3, Application US/09813918

; Patent No. 6383789

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al.

; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001175

; CURRENT APPLICATION NUMBER: US/09/813,918

; CURRENT FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 288
; TYPE: PRT
; ORGANISM: Human
US-09-813-918-3

Query Match 18.2%; Score 503.5; DB 4; Length 288;
Best Local Similarity 35.9%; Pred. No. 3.7e-45;
Matches 104; Conservative 53; Mismatches 126; Indels 7; Gaps 4;

Qy 234 RP-VLSHLLKAEWFINSDFAFDFARPLLNTVYVGGIMEKPIKPVPQDLENFIAKFGD 292
|| | : ||::| : : ::| | | || :|| | ||:|::| | : | :
Db 1 RPTTLFETMGKADIWLMRNSWSFQFHPFLPNVDFVGGFHCCKPAKPLPKEMEETFVQSSGE 60

Qy 293 SGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQGVWKCQCSEHWPDKVHLAANVKIVDWL 352
:| | : ||::| : | : | | :|| |::| : | | | : : | :
Db 61 NGVVVFSLSGVISN-MTAERANVIATALAKIPQKVLWRFDGN---KPDALGLNTRLYKWI 116

Qy 353 PQSDLLAHPsirLfvthGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQL 412
||:||| || | |:|||| | | || |::|||||| |::|: :::| | :
Db 117 PQNDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGIPLFFDQPDNIAHMKAKGAARLDF 176

Qy 413 KKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLK 472
: : | :| ::| || : | | | : | | | | : | : || ||:
Db 177 NTMSSTDLLNALKTVINDPLYKENIMKLSRIQHDQPVKPLDRAVFWIEFVMPHKGAKHLR 236

Qy 473 PYVFQQPWHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLARGARKVKE 522
| : : || ||| :::| | : ||| | :
Db 237 VAAHDLTWfQYHSLDVIGFLLACVATVIFIITKfCLFCFW--KFARKGKK 284

RESULT 12

US-09-305-856B-18

; Sequence 18, Application US/09305856B
; Patent No. 6479236
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; TITLE OF INVENTION: Genotyping the Human
; TITLE OF INVENTION: UDP-Glucuronosyltransferase 1 (UGT1). Gene
; FILE REFERENCE: 4389-7 (formerly SEQ-17CIP)
; CURRENT APPLICATION NUMBER: US/09/305,856B
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/084,807
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-305-856B-18

Query Match 13.7%; Score 380; DB 4; Length 245;
Best Local Similarity 34.8%; Pred. No. 4.5e-32;
Matches 78; Conservative 49; Mismatches 93; Indels 4; Gaps 2;

Qy 282 DLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQGVWKCQCSEHWPDKVH 341

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      : | : | | : | | : : | | | : : : : : : : :
Db      1 EFEAYINASGEHGIVVFSLGSVMSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSN 56

Qy      342 LAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRV 401
      | | | : | | | | : | | | | : : | : | : | | | : | | :
Db      57 LANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMPLFGDQMDNAKRM 116

Qy      402 EAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDH 461
      | | | | : : : : : | | : | : | | : : : | : | | : :
Db      117 ETKGAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEF 176

Qy      462 VLQTTGATHLKPYVFPQWHEQYLFDFVFLGLTLGLTLWLTCGK 505
      | : | | | : | | : : | | | : | : : |
Db      177 VMRHKGAPHLRPAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 220

```

RESULT 13

US-08-942-012B-32

```

; Sequence 32, Application US/08942012B
; Patent No. 6235278
; GENERAL INFORMATION:
; APPLICANT: Miller, Lois K.
; APPLICANT: Lu, Albert
; APPLICANT: Dierks, Peter
; APPLICANT: Black, Bruce
; TITLE OF INVENTION: Biological Insect Control Agents Expressing
; TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions
; FILE REFERENCE: 28-96a
; CURRENT APPLICATION NUMBER: US/08/942,012B
; CURRENT FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: 08/729,606
; PRIOR FILING DATE: 2000-10-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Spodoptera littoralis nuclear polyhedrosis virus
US-08-942-012B-32

```

```

Query Match          12.5%; Score 346.5; DB 3; Length 515;
Best Local Similarity 22.5%; Pred. No. 5.9e-28;
Matches 122; Conservative 102; Mismatches 211; Indels 107; Gaps 18;

```

```

Qy      20 SEAAKILTI-STVGGSHYLLMDRVSQILQDHGHNVMTL-----NHKRGPFMPDFKKEEKS 73
      | | : : | : | | : | | | : : | | |
Db      16 SAAVRVLCMFPTPSYSHQTVFDVYVNALLRRGHSLVVISPKIHNNHNG----- 63

Qy      74 YQVISWLAPEDHQREFKKSFD-----FF---LEETLGGRGK-----FENLLNV 113
      | : | | | | | | : : | : | :
Db      64 -----HRHHRHENLTEIDVGSVTNNFFKRLQLQDSKVSRRKGIVSDSSTVTRVNYLGL 115

Qy      114 LEYLALQCSHFILNRKDIMDSLK-NENFDMVIVETFDCPFLIAEKLKGPFFVAILSTSFGS 172
      : : | | : : | : | | : : | | : : | : | :
Db      116 ARMISAQFEH---EQVKRLLRSNQTFDVIVIEAFVSYPLILSYFFKDTPIQISSGHGT 171

Qy      173 LEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTE- 231

```

```

      |           : : | |   : :   | :   :   | : : |||
Db    172 AE-----NFETMGAVARHPVYYPNMWRDRFKGLSVWQTVRQVFTEI 212

Qy    232 -----GSR-PVLSHLLKAEIWFINSDFAFDFARPLLNTVYVG 269
      ||: | : |   : | : |   || ||: | | :|
Db    213 RLYMEFSQLDADQSAMMKRQFGSKVPDVALRKNVHMMFVNTHPVFDTNRPVPSNVQYLG 272

Qy    270 GL-MEKPIKPVPQDLENFIAKFGDS---GFVLVTLGSMVNTCQNPEIFKEMNNAFAH--- 322
      | : : : | : : | : | : : | | | : | |   : :   | | |
Db    273 GIHIDPAVTSVADEIDNDLAEFLENSTMGVVYVSLGSSVRA---SDMDSNMLNVFVETFR 329

Qy    323 -LPQGVIIWKQCQSHWPKDVHLAANKIVDWLPQSDLLAHPsirLFVTHGGQNSIMEAIQH 381
      : | | : | |   | : : | | | | | : | | : : : | | | | | |
Db    330 SIPYRVLWKVDKSDKIFD-NIPSNVLIQRWFPQRRVLKHRNVKVFITQGGVQSTDEAIDA 388

Qy    382 GVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAAS 441
      ||| | : | : | | | : | |   | :   : | |   : : : : | : :
Db    389 GVPMFGVPIMGDQFYNVMYETYGIGRGVDTLTVDARQLTEIVMDVADNEKYKNGTLWLR 448

Qy    442 VILRSHPLSPTQRLVGWIDHVLQTGGA-THLKPYPVFQPPWHEQYLFDFVFLGLTLGLTL 500
      : | : | : : | : : | | | |   : : : | : : : | : : :
Db    449 DAIMDQPMRPLEKAVWYTEHVARRKGAKKHLGTRAANVTYSKYAMFDLILPML-ITIFST 507

Qy    501 WL 502
      : |
Db    508 YL 509

```

RESULT 14

US-08-942-012B-33

; Sequence 33, Application US/08942012B

; Patent No. 6235278

; GENERAL INFORMATION:

; APPLICANT: Miller, Lois K.

; APPLICANT: Lu, Albert

; APPLICANT: Dierks, Peter

; APPLICANT: Black, Bruce

; TITLE OF INVENTION: Biological Insect Control Agents Expressing

; TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions

; FILE REFERENCE: 28-96a

; CURRENT APPLICATION NUMBER: US/08/942,012B

; CURRENT FILING DATE: 1997-10-01

; PRIOR APPLICATION NUMBER: 08/729,606

; PRIOR FILING DATE: 2000-10-01

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 33

; LENGTH: 460

; TYPE: PRT

; ORGANISM: Lacanobia oleracea granulovirus

US-08-942-012B-33

Query Match 12.4%; Score 342.5; DB 3; Length 460;

Best Local Similarity 24.7%; Pred. No. 1.3e-27;

Matches 120; Conservative 93; Mismatches 215; Indels 57; Gaps 18;

Qy 7 LLLVGFLPGVLLSEAAKILTI-STVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65

```

      :||:  :  :|  | || :  |  || :  |  ||||:  |
Db      5 ILLLALAVERIL---CANILCVFPTPAYSHQSVFSAYIDKLSWAGHNVTVIT-----P 54

Qy      66 DFKKEEKSYQVISWLAPEDHQREFK-----KSFDFLEETLGGRGKFENLLNVLEYLALQ 120
      :  :  :||:| |:  |  |  :||  :  :  |:|:
Db      55 MPRAVDHVHQVSSLSVHYFNNLIKNSTMIKKRGVVADETTVTKENYMGLINLV----- 108

Qy      121 CSHFLNRKDIMDSLKNE--NFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLP 178
      :| :  ::  |:|:  ||::|  |  ::  |  ||  |
Db      109 -AHEIKSPNVTRLRLRNKGKFDLIVCEA--YVSYILV-----FGAIYDAPVIQFSSGYA 159

Qy      179 IPLSYVPVFRSLLTDHM---DFWG---RVKNF--LMFFSFCRRQ-QHMQSTFDNTIKEHF 229
      || ::  |  :  |:  :  |  ||  ||  ::  :  :  :| :| |
Db      160 IPENFETVGGEVARNHIKHPNIWRSDFSKSNFEQLMTENYLKNEWALLEKEQENMLKRDF 219

Qy      230 TEGSRPVLSHLLLKAELWFINSDFAFDFARPLLPTVYVGGL-MEKPIKPVPQDLENFIA 288
      |  :  |  :  :||  ||  |  :  |  |:|:  ::||  | :|:
Db      220 --GYHHDMCQLKSRVLMFLINPAVFDNNRDVSNNIQYLGGIHLKKPRTVRDSRLLSFME 277

Qy      289 KFGDSGFVLVTLGSMVNTC-QNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHL----A 343
      |  |  :  || ::  :  :  |  |  :|  |:|  |  :||  :
Db      278 K--HHIIVYASFGSGIDVLNMDANLIAEFVRVFNNSIPYAVLWKVDSS-----IHLKHNIS 330

Qy      344 ANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEA 403
      :||  |  || |:| || |:|:| ||  |  ||:  |||:| |:| | :|
Db      331 SNVHTQSWFPQRDVLNHPHIKVFITQGGVQSTDEAVNSGVPMIGIPIMGDQFYNVRRYTE 390

Qy      404 KKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVL 463
      |  :  :|:| |  |:| :: :| |  :  :  :|  | :| :| :| :| :|
Db      391 LGIGEKVNILRLEEGLDRKIKNLVHNKSYELNIKRLNLFISDTPVKPLRKALWFTNYVL 450

Qy      464 QTGGA 468
      :  |
Db      451 RNKDA 455

```

RESULT 15

US-08-942-012B-24

; Sequence 24, Application US/08942012B

; Patent No. 6235278

; GENERAL INFORMATION:

; APPLICANT: Miller, Lois K.

; APPLICANT: Lu, Albert

; APPLICANT: Dierks, Peter

; APPLICANT: Black, Bruce

; TITLE OF INVENTION: Biological Insect Control Agents Expressing

; TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions

; FILE REFERENCE: 28-96a

; CURRENT APPLICATION NUMBER: US/08/942,012B

; CURRENT FILING DATE: 1997-10-01

; PRIOR APPLICATION NUMBER: 08/729,606

; PRIOR FILING DATE: 2000-10-01

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 515

; TYPE: PRT

; ORGANISM: Helicoverpa zea nuclear polyhedrosis virus
US-08-942-012B-24

Query Match 11.6%; Score 321; DB 3; Length 515;
Best Local Similarity 24.4%; Pred. No. 3.2e-25;
Matches 129; Conservative 88; Mismatches 246; Indels 66; Gaps 21;

```
Qy      6 VLLLVGFLLPGVLLSEAAKILTISTVGG-SHYLLMDRVSQILQDHGHNVTMLNHKRGPFM 64
      :| | | | | | | | | : | : | : | | : : : : | | : : | |
Db      8 MLLLVLFL--SVL--DGARILCVFPVPSYSHHAVFEAYTNALASRGHTIVRIT----PF- 58

Qy     65 PDFKKEEKSYQVISWLAPEDH-----QREFKKSFDFFLEETLGGRGKFENLLNVLEYL 117
      | | : : : : : | : | | | | | | | : | | : |
Db     59 PTKKNDSSNVTDVDVLSKDYFKSLVDRSRLFKK-----RGVISETSSVTARN 106

Qy    118 ALQCSHFLNRKDIMDSLK-----NENFDMVIVETF-DYCPFLIAEKLKG-PFVAI----- 165
      : | | : : : : | | : : | | | | : : | | : |
Db    107 YISLVHMLIDQFSVESVRQLIESNNVFDLLVTEAFLDY-PLVFSHLFGDVPVIQISSGHA 165

Qy    166 LSTSFGSLEFGLPIPLSYVPVFRSLTDMDFWGRV---KNFLMFFSFCRRQOQHMOSTF 221
      | : : : : | : | : : : : : : : : : : | |
Db    166 LAENFETMGAVSRHPPIYYPNLWRNKF-QNLNVWEIITEIYTELVLYLEFARLADE----- 219

Qy    222 DNTIKEHFTEGSRPVLSHLLLKAEWFINSDFAFDFARPLLENTVYVGGLMKPIKPV-- 279
      : | : : | : : | : : | : : | | | : : | : | | |
Db    220 QTKMLRHQFGPNTPSVEELRQVRQLLFVNTHPLFDNNRPVPPSVQYLGSLHLDRNNDVDE 279

Qy    280 PQDLENFIAKF---GDSGFVLVTLGSMVNTC-QNPEIFKEMNNAFAHLPQGVWKCQCSH 335
      | : : : : | : | | : : : : : | | | | : : |
Db    280 QQTMDYNLMQFLNNSTNGVVYVSFGTSIRVSDMDDEFLFEFITAFAKQLPYNILWK--TDG 337

Qy    336 WPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQP 395
      | : | | | | | | : | : : | | | | | | | | : : | | | |
Db    338 MPMEHVLPKNVLTQTWLPQHHVLKHSNVVAFVTQGGMQSTDEAIDACVPLIGIPFMGDQA 397

Qy    396 ENMVRVEAKKFGVSIQLKKLKAETL--ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQ 453
      | : | | : : | : | | : : | | | : : | : |
Db    398 YNTNKYEELGIGRNLDPVTLTSHILVSAVLDTVNNKSRYTDNIKALNRSTNYRTRKPM 457

Qy    454 RLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDDVFV----FLLGLTLG 498
      : : : : | : | | : : | : | : | | : | |
Db    458 KAIWYTEHVIDNGKNPILKTKAANVSYSKYMSDIIVPVITFLVMTHLG 506
```

Search completed: May 7, 2004, 17:33:56
Job time : 23 secs

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:29:09 ; Search time 21 Seconds
 (without alignments)
 2395.627 Million cell updates/sec

Title: US-10-017-867A-282
 Perfect score: 2768
 Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWVWLRGARKVKET 523

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query			Description
	Score	Match	Length	DB	ID	
1	700	25.3	541	2	JC5423	2-hydroxyacylsphin
2	684	24.7	541	2	A48801	2-hydroxyacylsphin
3	679	24.5	533	2	A39092	glucuronosyltransf
4	674.5	24.4	530	2	A40467	glucuronosyltransf
5	671	24.2	529	2	A42233	glucuronosyltransf
6	670	24.2	531	2	B47113	glucuronosyltransf
7	662.5	23.9	530	2	C47113	glucuronosyltransf
8	658	23.8	531	2	A35343	glucuronosyltransf
9	658	23.8	535	2	I57961	glucuronosyltransf
10	656.5	23.7	528	2	JN0619	glucuronosyltransf
11	654.5	23.6	529	2	A35366	glucuronosyltransf
12	650	23.5	527	2	S15089	glucuronosyltransf
13	649	23.4	530	2	A48633	glucuronosyltransf

14	642	23.2	528	2	JN0620	UDP-glucuronosyltr
15	640	23.1	530	2	S07390	glucuronosyltransf
16	639	23.1	530	2	A36276	glucuronosyltransf
17	637.5	23.0	530	2	S00163	glucuronosyltransf
18	632.5	22.9	530	2	S68200	glucuronosyltransf
19	632	22.8	523	2	S11309	glucuronosyltransf
20	629	22.7	531	2	A31340	glucuronosyltransf
21	623	22.5	530	2	JC5656	UDP glucuronosyltr
22	622.5	22.5	529	2	JE0200	orphan UDP-glucuro
23	612.5	22.1	531	2	A55788	glucuronosyltransf
24	610	22.0	530	2	S17512	glucuronosyltransf
25	600	21.7	529	2	A24600	glucuronosyltransf
26	596.5	21.5	531	2	B55788	glucuronosyltransf
27	513	18.5	485	2	T13694	glucuronosyltransf
28	471	17.0	949	2	T18591	hypothetical prote
29	455.5	16.5	534	2	T34455	hypothetical prote
30	449	16.2	531	2	T33980	hypothetical prote
31	448	16.2	573	2	T27578	hypothetical prote
32	447	16.1	531	2	T23835	hypothetical prote
33	441.5	16.0	508	2	T03910	UDP-glucuronosyltr
34	438	15.8	534	2	T19944	hypothetical prote
35	427	15.4	586	2	T19075	hypothetical prote
36	424	15.3	534	2	T19951	hypothetical prote
37	419	15.1	533	2	T34458	hypothetical prote
38	412.5	14.9	475	2	T33979	hypothetical prote
39	412.5	14.9	537	2	T25536	hypothetical prote
40	411	14.8	745	2	T23893	hypothetical prote
41	409.5	14.8	661	2	T32518	hypothetical prote
42	408	14.7	533	2	T34457	hypothetical prote
43	405.5	14.6	520	2	T19661	hypothetical prote
44	405	14.6	530	2	T18596	hypothetical prote
45	398.5	14.4	526	2	T25535	hypothetical prote

ALIGNMENTS

RESULT 1

JC5423

2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) - human

N;Alternate names: UDP-galactose:ceramide galactosyltransferase

C;Species: Homo sapiens (man)

C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999

C;Accession: JC5423

R;Kapitonov, D.; Yu, R.K.

Biochem. Biophys. Res. Commun. 232, 449-453, 1997

A;Title: Cloning, characterization, and expression of human ceramide galactosyltransferase cDNA.

A;Reference number: JC5423; MUID:97242209; PMID:9125199

A;Accession: JC5423

A;Molecule type: mRNA

A;Residues: 1-541 <KAP>

A;Cross-references: GB:U62899

A;Experimental source: fetal glioma cell

C;Comment: This enzyme catalyzes the final step of galactosylceramide synthesis.

C;Genetics:

A;Gene: cgt

C;Superfamily: glucuronosyltransferase

C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

F;472-492/Domain: hydrophobic #status predicted <HYD>

F;538-540/Region: endoplasmic reticulum retention signal #status atypical

F;78,333,442/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.3%; Score 700; DB 2; Length 541;
Best Local Similarity 32.2%; Pred. No. 6.5e-47;
Matches 166; Conservative 95; Mismatches 185; Indels 70; Gaps 12;

```
Qy      13 LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70
      |  | ::|||: :  :  ||  :  ::  | : ||: | :|: |
Db      11 LWSAVGIAKAAKIIIVPPIMFESHMYIFKTLASALHERGHHTVFLLEGRD----- 61

Qy      71 EKSQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119
      :|| :|  : :  |  | ||: :  ||  | :||:
Db      62 -----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAIELFDILDHYTK 112

Qy     120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFAVAILSTSFGSLEFGLPI 179
      |  :  ::  || | ||::|: | | |:||  ||  :  :  :  | | |
Db     113 NCDMMVGNHALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172

Qy     180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQHM-----QSTFD 222
      ||:| | | | | | | :  | :||  ||:  : | |  : | :|
Db     173 PLAYVPEFNSLLTDRMNLQRMKNTGVYLISRLGVSFLVLPKYERIMQKYNLLPEKSMYD 232

Qy     223 NTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQD 282
      | :  : || : :| | :| || || | ||| : : ||  | :|:|
Db     233 -----LVHGSSLWMLCTDVALEFFRPTLPNVVYVGILTKPASPLPED 275

Qy     283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHL 342
      | : ::  : ||||: | : |  : :| : : |  || | ||:  ||  : |
Db     276 LQRWVNGANEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFS---GPKPKNL 331

Qy     343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPPLFGDQPENMVRVE 402
      | |:::| |||: || |  | : ||: || | | : | |||: |||: |||  : | ||:
Db     332 GNNTKLI EWLPQNDLLGHGSKIAFVSHGGLNSIFETMYHGVPPVVGIPVFGDHYDTMTRVQ 391

Qy     403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      || | : :: | :  : |  : :: :  | :  |  | :  |  |  | : |||:
Db     392 AKGMGILLEWKTVTEKELYEALVKVINNPYSYRQRAQKLSEIHKDQPGHPVNRTIYWIDYI 451

Qy     463 LQTGGATHLKPYPVFQQPWHEQYLFQV-FVFLGLTL 497
      : : || ||: | |  : : :| | : || || |
Db     452 IRHNGAHLRAAVHQISFCQYFLLDIAFVLLLGAAL 487
```

RESULT 2

A48801

2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) precursor - rat

N;Alternate names: UDPgalactose-ceramide galactosyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A48801; I56576; S63480

R;Schulte, S.; Stoffel, W.

Proc. Natl. Acad. Sci. U.S.A. 90, 10265-10269, 1993

A;Title: Ceramide UDPgalactosyltransferase from myelinating rat brain: purification, cloning, and expression.
A;Reference number: A48801; MUID:94052143; PMID:7694285
A;Accession: A48801
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-541 <SCH>
A;Cross-references: GB:L21698; NID:g437665; PIDN:AAA16108.1; PID:g437666
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:139520, NCBIP:139522)
R;Stahl, N.; Jurevics, H.; Morell, P.; Suzuki, K.; Popko, B.
J. Neurosci. Res. 38, 234-242, 1994
A;Title: Isolation, characterization, and expression of cDNA clones that encode rat UDP-galactose:ceramide galactosyltransferase.
A;Reference number: I56576; MUID:94358923; PMID:7521399
A;Accession: I56576
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-541 <RES>
A;Cross-references: EMBL:U07683; NID:g464025; PIDN:AAA50212.1; PID:g464026
R;Schulte, S.; Stoffel, W.
Eur. J. Biochem. 233, 947-953, 1995
A;Title: UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter: copurification, separation and characterization of the two glycoproteins.
A;Reference number: S63480; MUID:96085162; PMID:8521863
A;Accession: S63480
A;Molecule type: protein
A;Residues: 21-28,'A',30-31,'Q',33-39;73-77,'X',79-87;155-166,'Q',168-173;315-322;330-331,'EX',334-338,'Q',340-353;416-423;510-515 <SUL>
A;Experimental source: brain
C;Function:
A;Description: transfers galactose from UDP-galactose to ceramide
C;Superfamily: glucuronosyltransferase
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-541/Product: 2-hydroxyacylsphingosine 1-beta-galactosyltransferase #status experimental <MAT>
F;78,333/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 24.7%; Score 684; DB 2; Length 541;
Best Local Similarity 32.2%; Pred. No. 1.2e-45;
Matches 165; Conservative 94; Mismatches 184; Indels 70; Gaps 12;

Qy	13	LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE	70
		: : : : : : : : : :	
Db	11	LWSAVGIARAAKIIIVPPIMFESHLYIFKTLASALHERGHHTVFLLEGRD-----	61
Qy	71	EKSQYQVISWLPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL	119
		: : : : : : : : : : : :	
Db	62	-----IDPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAVELVDILDHYTK	112
Qy	120	QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAILSTSFGSLFGLPI	179
		: : : : : : : : : :	
Db	113	NCDMMVGNQALIQLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA	172
Qy	180	PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH-----MQSTFD	222

```

      ||: || | |||| | : | | : ||      ||:  : | |      : | : |
Db      173 PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRMGVSFVLVLPKYERIMQKYNLLPAKSMYD 232
Qy      223 NTIKEHFTEGSRPVLSHLLKAEWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQD 282
      | :  : || : : | | : | || ||| |||| : | | | : | : |
Db      233 -----LVHGSSLWMLCTDVALEFPRPTLPNVVYVGGILTKPASPLPED 275
Qy      283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQC SHWPKDVHL 342
      | : : :  : |||| : | : |  : : | : | ||| ||| :  :  | : |
Db      276 LQRWVDGAQEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---KPKNL 331
Qy      343 AANVKIVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVE 402
      | | : : |||| : || | : || | ||| | : | ||| : ||||| | : | || :
Db      332 GNNTKLIEWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVVVGIPLFQGDHYDTMTRVQ 391
Qy      403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      || | : : :  |  : : : : | : | | | : | | | | ||| :
Db      392 AKGMGILLEWNTVTEGELYDALVKVINNP SYRQRAQKLSEIHKDQPGHPVNRRTTYWIDYI 451
Qy      463 LQTGGATHLKPYVFQQPWHEQYLFQDV-FVFLLG 494
      | : || || : | | : : : | | : || || |
Db      452 LRHDGAHHLRS AVHQISFCQYFLLDIAFVLLLG 484

```

RESULT 3

A39092

glucuronosyltransferase (EC 2.4.1.17) 1 precursor, bilirubin-specific - human
N;Alternate names: bilirubin UDP-glucuronosyltransferase

C;Species: Homo sapiens (man)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 29-Sep-1999

C;Accession: A39092; E42586; A48887

R;Ritter, J.K.; Crawford, J.M.; Owens, I.S.

J. Biol. Chem. 266, 1043-1047, 1991

A;Title: Cloning of two human liver bilirubin UDP-glucuronosyltransferase cDNAs
with expression in COS-1 cells.

A;Reference number: A39092; MUID:91093210; PMID:1898728

A;Accession: A39092

A;Molecule type: mRNA

A;Residues: 1-533 <RIT>

A;Cross-references: GB:M57899; NID:g184472; PIDN:AAA63195.1; PID:g184473

R;Ritter, J.K.; Chen, F.; Sheen, Y.Y.; Tran, H.M.; Kimura, S.; Yeatman, M.T.;
Owens, I.S.

J. Biol. Chem. 267, 3257-3261, 1992

A;Title: A novel complex locus UGT1 encodes human bilirubin, phenol, and other
UDP-glucuronosyltransferase isozymes with identical carboxyl termini.

A;Reference number: A42586; MUID:92147680; PMID:1339448

A;Accession: E42586

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-288 <RI2>

A;Cross-references: GB:M84125; NID:g340131; PIDN:AAA61248.1; PID:g340132

A;Note: sequence extracted from NCBI backbone (NCBIP:81433)

R;Ritter, J.K.; Yeatman, M.T.; Kaiser, C.; Gridelli, B.; Owens, I.S.

J. Biol. Chem. 268, 23573-23579, 1993

A;Title: A phenylalanine codon deletion at the UGT1 gene complex locus of a
Crigler-Najjar type I patient generates a pH-sensitive bilirubin UDP-
glucuronosyltransferase.

A;Reference number: A48887; MUID:94043159; PMID:8226884
 A;Accession: A48887
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 161-170,172-180 <RI3>
 A;Experimental source: liver, Crigler-Najjar type I patient
 A;Note: sequence extracted from NCBI backbone (NCBIP:138934)
 C;Genetics:
 A;Gene: GDB:UGT1A1; UGT1
 A;Cross-references: GDB:120007; OMIM:191740
 A;Map position: 2q37-2q37
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.5%; Score 679; DB 2; Length 533;
 Best Local Similarity 33.8%; Pred. No. 2.8e-45;
 Matches 175; Conservative 93; Mismatches 211; Indels 38; Gaps 13;

Qy	8	LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP	65
		:: :: : ::	
Db	11	LVLGLLLCVLGPVVS HAGKILLI-PVDGSHWLSMLGAIQQLQQRGHEIVVL-----AP	62
Qy	66	D---FKKEEKSYQVISWLAPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL	111
		: :: : :: :: : : :::	
Db	63	DASLYIRDGAFTYTLKTY--PVPFQREDVKESFVSLGHNVFENDSFLQRVI---KTYKKIK	117
Qy	112	NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFG	171
		: :: : ::: :: :	
Db	118	KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC	177
Qy	172	SLEF---GLPIPLSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH	228
		: : : : :	
Db	178	SLEFEATQCPNPFYSYVRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE	236
Qy	229	FTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKPKVPQDLENFIA	288
		: : : : :: : :: : : :	
Db	237	FLQ-REVTVQDLLSSASVWLFERSDFVKDYPRPIMPNMVVFVGGINCLHQNPLSQEFEAYIN	295
Qy	289	KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKI	348
		: : : ::: : : : : : : : : : :	
Db	296	ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLANTIL	351
Qy	349	VDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLFQDQPENMVRVEAKKFGV	408
		: : : : : : : : :	
Db	352	VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFGDQMDNAKRMETKGAGV	411
Qy	409	SIQLKKLKAETLALKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA	468
		:: : :: : : :: : : : : : : : :	
Db	412	TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKA	471
Qy	469	THLKPYVFQQPWHEQYLFDFVFVFLGLTLGLTLWLCCGK	505
		: ::: : ::	
Db	472	PHLRPAADLTWYQYHSLDVIGFLLAVVLTVAFITFK	508

glucuronosyltransferase (EC 2.4.1.17) precursor - rat
N;Alternate names: UDP-glucuronosyltransferase isoform 53K
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 17-Nov-2000
C;Accession: A40467; A23520; S59627; A26064; I55247
R;Haque, S.J.; Petersen, D.D.; Nebert, D.W.; Mackenzie, P.I.
DNA Cell Biol. 10, 515-524, 1991
A;Title: Isolation, sequence, and developmental expression of rat UGT2B2: the gene encoding a constitutive UDP glucuronosyltransferase that metabolizes etiocholanolone and androsterone.
A;Reference number: A40467; MUID:91369480; PMID:1909872
A;Accession: A40467
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-530 <HAQ>
R;Jackson, M.R.; Burchell, B.
Nucleic Acids Res. 14, 779-795, 1986
A;Title: The full length coding sequence of rat liver androsterone UDP-glucuronyltransferase cDNA and comparison with other members of this gene family.
A;Reference number: A23520; MUID:86120371; PMID:3003696
A;Accession: A23520
A;Molecule type: mRNA
A;Residues: 31-158,'E',160-285,'S',287-350,'I',352-362,'I',364-430,'E',432-530 <JAC>
A;Cross-references: GB:X03478; NID:g57452; PIDN:CAA27198.1; PID:g57453
A;Note: the authors translated the codon ATT for residue 321 as Asn
R;Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugiura, T.; Waku, K.
Biochem. J. 312, 301-308, 1995
A;Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of rat liver: their effect on enzyme activity.
A;Reference number: S59626; MUID:96077159; PMID:7492328
A;Accession: S59627
A;Molecule type: protein
A;Residues: 24-44 <YAM>
R;Mackenzie, P.I.
J. Biol. Chem. 261, 14112-14117, 1986
A;Title: Rat liver UDP-glucuronosyltransferase. cDNA sequence and expression of a form glucuronidating 3-hydroxyandrogens.
A;Reference number: A26064; MUID:87033594; PMID:2429951
A;Accession: A26064
A;Molecule type: mRNA
A;Residues: 1-430,'E',432-530 <MAC>
A;Cross-references: GB:J02589; NID:g207582; PIDN:AAA42314.1; PID:g207583
A;Experimental source: hepatic
C;Superfamily: glucuronosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-530/Product: glucuronosyltransferase #status experimental <MAT>

Query Match 24.4%; Score 674.5; DB 2; Length 530;
Best Local Similarity 33.5%; Pred. No. 6.3e-45;
Matches 170; Conservative 86; Mismatches 219; Indels 33; Gaps 13;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSQVISW-LAPEDHQREFKKS 92
||::: : | ||||: | : :: | :::: | |
Db 34 SHWMNIKIILDELVQRGHEVTVLKPSAYFFLDPKKSSDLKFEIFSTSIKDELQNHFIKL 93

Qy	93	FDFFLEE-----TLGGRGKFENLLNVLEYLALQ-CSHFLENRKDIMDSLKNENFDMVIVET	146
Db	94	LDVWTYELPRDTCLSYSPILQNLVYEFSYFYLSICKDAVSNKQLMTKLQESKFDVLFADP	153
Qy	147	FDYCPFLIAEKLGPVFAILSTSFSG-SLEFGLP---IPLSYVPVFRSLLTDHMDFWGRVK	202
Db	154	VASCGDLIAELLHIPFLYSLSFSPGHKLEKSIGKFILPPSYVPVILSGLAGKMTFIDRVK	213
Qy	203	NF--LMFFSF-CRRQQHMQ-STFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFA	258
Db	214	NMICMLYFDFWFERLRHKEWDTFYSEIL-----GRPTTVDETMKSKEIWLIRSYWDLKFP	268
Qy	259	RPLLNTVYVGGLMKEPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN	318
Db	269	HPTLPNVDIYIGGLHCKPAKPLPKDMEEFVQSSGEHGVVVFSLGSMVS-----NMTEEKAN	323
Qy	319	----AFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQNS	374
Db	324	AIAWALAQIPQKVLWKFD---GKTPATLGPNTRVYKWLPQNDLLGHPKTKAFVTHGGANG	380
Qy	375	IMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK	434
Db	381	LYEAIYHGIPMIGIPLFGDQPDNIAHMAKGAASVSLNIRTMSKLDFLSALVEVIDNPFYK	440
Qy	435	SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLLG	494
Db	441	KNVMLLSTIHHDQPMKPLDRAVFWIEFIMRHKGAKHLRPLGHNLPWYQYHSLDVIGFLLT	500
Qy	495	LTLGTLWLWCGK-LLGMAVWWLRGARKVK	521
Db	501	CFAVIAALTVKCLLFMYRFFVKKEKKMK	528

A;Accession: A24324
A;Molecule type: mRNA
A;Residues: 1-407, 'V', 409-529 <MA2>
A;Cross-references: GB:M13506; NID:g207580; PIDN:AAA42313.1; PID:g207581
A;Experimental source: liver
C;Superfamily: glucuronosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.2%; Score 671; DB 2; Length 529;
Best Local Similarity 32.2%; Pred. No. 1.2e-44;
Matches 175; Conservative 90; Mismatches 228; Indels 50; Gaps 15;

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Qy      6 VLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
      ::|: : ||      |:| | ||: : : | || |:| :
Db      11 LIQLICYFRPGA----CGKVLVWPT-EYSHWINIKIILNELAQRGHEVTVLVSSASILIE 65

Qy      66 DFKKEEKSYQVISW-LAPEDHQREFKKSFDFFLE--ETLG---GRGKFENLLN---VLE 115
      |:  :::: | |: | : | | : |||      | : : | |:|
Db      66 PTKESSINFEIYSVPLSKSDLEYSFAKWIDEWTRDFETLSIWTYYSKMQKVFNEYSDVVE 125

Qy      116 YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFG---- 171
      | | : |:| |: ||::: : | |:|| | | | | |
Db      126 NL---CKALIWNKSLMKKLQGSQFDVILADAVGPCGELLAELLKTPLVYSLRFCPGYRCE 182

Qy      172 SLEFGLPIPLSYVPVFRSLTLDHMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHF 229
      |||:| |||| | |:| | | ||| | ::| | | : : : :
Db      183 KFSGGLPLPPSYVPVVLSELSDRMTFVERVKNMLQMLYFDF-----WFQPFKEKSWSQFY 237

Qy      230 TE--GSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQDLENFI 287
      :: | |: :: ||::| | : : : | || | ||| :||| || ||:::| |:
Db      238 SDVLGRPTTLTEMMGKADIWLIRTFWDLEFPHFPLPNFDFVGGGLHCKPAKPLPREMEEFV 297

Qy      288 AKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShwPKDVHLAANVK 347
      |: | |: :||| | | : :| | :|| |:| : | | :| :
Db      298 QSSGEHGVVVFSLGSMVKNL-TEEKANVVASALAQIPQKVVRFD---GKKPDTLGSNTR 353

Qy      348 IVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFG 407
      : |:|:| | | | : || || | | || ||:|:| | | | | | | | | | :| |
Db      354 LYKWIPQNDLLGHPKTKAFVAHGGTNGIYEAIYHGPIVGIPLFADQPDNINHMBAKGAA 413

Qy      408 VSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGG 467
      | : | | : |:| | | | : | | | : | | | | | :| :| :
Db      414 VRVDFSILSTTGLLTALKIVMNDPSYKENAMRLSRIHHDQPVKPLDRAVFWIEYVMRHKG 473

Qy      468 ATHLKPYVVFQQPWHEQYLFDFVFVLLGLTLGT-----LWLCGKLLGMAVWWLRGARK 519
      | ||: : | : : || || : | | | | | | :|
Db      474 AKHLRSTLHDLSWFQYHSLDVIGFLLLCVGVVFIITKFCLECCRKTANM-----GKK 526

Qy      520 VKE 522
      ||
Db      527 KKE 529

```

RESULT 6

B47113

glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Sep-1999
 C;Accession: B47113
 R;Tukey, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tephly, T.R.
 J. Biol. Chem. 268, 15260-15266, 1993
 A;Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.
 A;Reference number: A47113; MUID:93315511; PMID:8325897
 A;Accession: B47113
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-531 <TUK>
 A;Cross-references: GB:L01081; NID:g165796; PIDN:AAA18020.1; PID:g165797
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.2%; Score 670; DB 2; Length 531;
 Best Local Similarity 32.6%; Pred. No. 1.4e-44;
 Matches 169; Conservative 90; Mismatches 206; Indels 54; Gaps 14;

```

Qy      34 SHYLLMDRVSQILQDHGHNVTML-----NHKRG----PFMPDFKKEEKSYQVISW 79
      ||:: | : | || ||:| |:: | | :::| : |
Db      35 SHWMNMKTILDALVQQGHEVTVLRSSASIVIGSNNESGIKFETFTSYRKDEIENFFMDW 94

Qy      80 LAPEDHQREFKKSFDFFLE---ETLGGRGKFENLLNVLEYLAL---QCSHFLNRKDIMDS 133
      :| :: :| || :::| : | : | :|
Db      95 F-----YKMIYNVSIESYWETFS-----LTKMVILKYSDICEDICKEVILNKKLMTK 141

Qy     134 LKNENFDMVIVETFDYCPFLIAEKLKGP-----FVAILSTSGSLEFGLPIPLSYVPV 186
      |: ||:: : |::| | | : : | ||:| ||||
Db     142 LQESRFDVVLADPVSPGGELLAELLKIPLVYSLRGFVGMYLQKHGG---GLLLPPSYVPV 198

Qy     187 FRSLTDMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHFTGSRPV--LSHLLLK 243
      | | | | ||:| | ::| | : : :| | || | :|
Db     199 MMSGGLGQMTEMERVQNLLCVLYDFW-FPKFNEKRWDQFYSEVL---GRPVTFLEIMGK 254

Qy     244 AELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSM 303
      |::| | | : :| ||||| :::| || ||:|:::|: | : | :|::|
Db     255 ADMWLIRSYWDLEFPRELLNFDFIGGLHCKPAKPLQEMEDFVQSSGEEGVVFSLGSM 314

Qy     304 VNTCQNPEIFKEMNNAFAHLPOGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPST 363
      :: | : :| | || |::: | | :| :: |:::| ||
Db     315 ISNL-TEERANVIASALALPQKVLWRFE---GKKPDMLGSNTRLYKWIPQNDLLGHPKT 370

Qy     364 RLFVTHGGQNSIMEAIQHGVPMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALK 423
      : |::| | : || |::|:::|::| :::| :::| | : || : : |
Db     371 KAFITHGGANGVFEAIYHGIPMVGPLPLFGDQLDNIVYMKAKGAVKLNLTMTSSADLLNA 430

Qy     424 MKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQ 483
      :| :: | || | : | | :| | | ||:|::| || ||: |::
Db     431 LKTVINDPSYKENAMTSLRIHHDQPMKPLDRAVFWIEYVMRHKGAKHLRVAHADLTWYQY 490

Qy     484 YLFDVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
      : || || | :| | : : || | |
Db     491 HSLDVIGFLLACVAITTYLIVKCLLVYRYVLGAGKKKK 529

```

C47113

Query Match 23.9%; Score 662.5; DB 2; Length 530;
Best Local Similarity 34.5%; Pred. No. 5.5e-44;
Matches 161; Conservative 75; Mismatches 209; Indels 21; Gaps 10;

Qy	50	GHNVTMLNHKRGPFMPDFDKKEEKSYQVISWLPAPEDHQRE-FKKSDFDFLEETLGGRGKFE	108
Db	51	GHEVIVLRNSASIFIDPSKQANIKFETFPIAATKDDLEDLFVHYVSTWTNARQNSQWKYF	110
Qy	109	NLLNVL--EY---LALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFV	163
Db	111	SL LQKLFSEYSDSCENACKEVVFNKTLMTKLQESRFDILLSDAIGPCGELLAELLKIPFV	170
Qy	164	AILSTSFG----SLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFL--MFFSFCRRQQHM	217
Db	171	YSLRFTPGYTMEKYSGGLSVPPSYVPIILSDLSGKMTFMERVNNMLCMLYFDFW-FQMFN	229
Qy	218	QSTFDNTIKEHFTEGSRPV-LSHLLLKAEIWFINSDFAFDFARELLPNTVYVGGLMKPI	276
Db	230	KKRWDQFYSEVL---GRPVTFSSELVGKADMWLIRSYWDLEFPRTPLNIQFVGGLHCKPA	286
Qy	277	KPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQCSHW	336
Db	287	KPLPKEMEETFVQSSGEEGVVVFSLGSMVSN-MTEERANLIASAFALPQKVIWRFD---G	342
Qy	337	PKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPE	396
Db	343	QKPETLGPNTRIYDWIPQNDLLGHPKTKAFVTHGGANGIYEAIHHGIPMVGLPLFGEQPD	402
Qy	397	NMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLV	456
Db	403	NIAHMTAKGAIRLNWKTMSSEDLNALKTVINDPSYKENVMTLSSIHHDQPMKPLDRAV	462
Qy	457	GWIDHVLQTGGATHLKPYPVFPQWPWHEQYLFDFVFLGLTLGLTLWL	502
Db	463	FWIEYVMRHKGAKHLRVAHDLTWFAQYHSLDVVGVFLVSCAAFLIFL	508

RESULT 8

A35343

glucuronosyltransferase (EC 2.4.1.17) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 29-Sep-1999

C;Accession: A35343

R;Sato, H.; Koiwai, O.; Tanabe, K.; Kashiwamata, S.

Biochem. Biophys. Res. Commun. 169, 260-264, 1990

A;Title: Isolation and sequencing of rat liver bilirubin UDP-

glucuronosyltransferase cDNA: possible alternate splicing of a common primary transcript.

A;Reference number: A35343; MUID:90274676; PMID:2112380

A;Accession: A35343

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-531 <SAT>

A;Cross-references: GB:M34007; NID:g207578; PIDN:AAA42312.1; PID:g207579

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 23.8%; Score 658; DB 2; Length 531;
Best Local Similarity 30.9%; Pred. No. 1.2e-43;
Matches 171; Conservative 106; Mismatches 211; Indels 66; Gaps 17;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
      : |   |||:  ||   :|  |:| :  : |||:| |  | : |   ||   :|
Db      7 LRGLSGLLLLLLALP---WAEGGKVL-VFPMEGSHWLSMRDVVRELHARGHQAVVL---- 58

Qy     61 GPFMPDFKKEEKSYQVISWLAP---EDHQREF----KKSFD-----FFLEETLGGRGK 106
      | :   | |  : : : : |   |::|||   || |:   ||  ||:   |
Db     59 APEVTVHMKGEDFFTLQTYAFPTYKKEYQREILGNAKKGFEPPQHVFVKTFE--ETMASIKK 116

Qy    107 FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGFVAIL 166
      | :|   |   | :  | :  : :  | : : ||:| :  :   | | : |  | | |
Db    117 FFDL-----YANSCAALLHNKTLIQQLNSSFDVVLTDVPVFPCGALLAKYLQIPAVFFL 170

Qy    167 STSFGSLEF---GLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFS---FCRRQQHMQST 220
      :   : :   | | ||:|   : : : ||| |  |||| |  :   |   | :  |
Db    171 RSVPCGIDYEATQCPKPSSYIPNLLTMSLDHMTFLQRVKNMLYPLTLKYIC----HLSIT 226

Qy    221 FDNTIKEHFTEGSR---PVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIK 277
      : :   :   :   ||||   | :|   || ||: ||: || | : : ||:   |
Db    227 PYESLASSELLQREMSLVEVLSH---ASVWLFRGDFVFDYPRPIMPNMVFIGGINCVIKK 282

Qy    278 PVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWP 337
      | : | : | : :   | : | | : : ||||:   :   | :  |   : || : : | :
Db    283 PLSQEFAYVNASGEHGIVVFSLSGSMVSEIPEKKAM-EIAEALGRIPQTLWRYTGT--- 338

Qy    338 KDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPEN 397
      :  : || |  : | ||||: ||| ||  | : || |  : | | | : |||| | : |||| | : |
Db    339 RPSNLAKNTILVKWLPQNDLLGHKPARAFITHSGSHGIYEGICNGVPMVMPLFGDQMDN 398

Qy    398 MVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVG 457
      | : | :  || : : : : | : |   : | : : : | |   :  | : :  | : |  |
Db    399 AKRMETRGAGVTNLNVEMTADDLENALKTVINNKSYPENIMRLSSLHKDRPIEPLDLAVF 458

Qy    458 WIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLGLGLTLGLWL-----CGKLLGM 509

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      |::|:: | | |::| |:: : | | | | : | :: | | |
Db      459 WVEYVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG- 517

Qy      510 AVWWLRGARKVKET 523
      | :|::
Db      518 -----GKGRVKKS 525

```

RESULT 9

I57961

glucuronosyltransferase (EC 2.4.1.17) precursor - rat

N;Alternate names: glucuronosyltransferase 1 B1; morphine UGT

C;Species: Rattus norvegicus (Norway rat)

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 29-Sep-1999

C;Accession: I57961; S51197; S68333

R;Coffman, B.L.; Green, M.D.; King, C.D.; Tephly, T.R.

Mol. Pharmacol. 47, 1101-1105, 1995

A;Title: Cloning and stable expression of a cDNA encoding a rat liver UDP-glucuronosyltransferase (UDP-glucuronosyltransferase 1.1) that catalyzes the glucuronidation of opioids and bilirubin.

A;Reference number: I57961; MUID:95327065; PMID:7603447

A;Accession: I57961

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-535 <RES>

A;Cross-references: EMBL:U20551; NID:g695161; PIDN:AAC52219.1; PID:g695162

R;Ishii, Y.; Tsuruda, K.; Tanaka, M.; Oguri, K.

Arch. Biochem. Biophys. 315, 345-351, 1994

A;Title: Purification of a phenobarbital-inducible morphine UDP-glucuronosyltransferase isoform, absent from guinea rat liver.

A;Reference number: S51197; MUID:95077409; PMID:7986077

A;Accession: S51197

A;Molecule type: protein

A;Residues: 30-41 <ISH>

R;Ikushiro, S.; Emi, Y.; Iyanagi, T.

Arch. Biochem. Biophys. 324, 267-272, 1995

A;Title: Identification and analysis of drug-responsive expression of UDP-glucuronosyltransferase family 1 (UGT1) isozyme in rat hepatic microsomes using anti-peptide antibodies.

A;Reference number: S68333; MUID:96132654; PMID:8554318

A;Accession: S68333

A;Molecule type: protein

A;Residues: 30-37 <IKU>

C;Genetics:

A;Gene: UGT1.1

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.8%; Score 658; DB 2; Length 535;

Best Local Similarity 31.4%; Pred. No. 1.3e-43;

Matches 171; Conservative 97; Mismatches 215; Indels 62; Gaps 14;

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Qy      13 LLPGVLL-----SEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
      | | | : | | | | : | | | | | | | | | | | : : |
Db      13 LLPCLLLCVLGPSASHAGKLLVI-PIDGSHWLSMLGVIQQLQKKGHEVVVI----APEAS 67

Qy      66 DFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFEN---LLNVLE----- 115

```

```

      || | : : | :: | : | || | : || ::
Db      68 IHIKEGSFYTMRKYPVPFQENENVTA-----FVEL---GRSVFDQDPFLLRVVKTYNKVKR 120
Qy      116 ---YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGS 172
      | || | : : | || : || : : | | : : | | | : |
Db      121 DSSMLLSGCSHLLHNAEFMASLEQSHFDALLTDPFLPCGSIVAQYLSLPAVYFLNALPCS 180
Qy      173 LEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFS---FCRRQQHMQSTFDNTIK 226
      | : | || || | | || | : | || | : : | | : |
Db      181 LDLEATQCPAPLSYVPKSLSSNTDRMNFLQRVKNMIIALTENFLCRVVYSPYGLATEIL 240
Qy      227 EHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENF 286
      : : || | : | : || | : || : || | : || : | : | :
Db      241 Q-----KEVTVKDLLSPASIWLMRNDVFKDYPRPIMPNMVFIGGINCLQKKALSQEFAY 295
Qy      287 IAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANV 346
      : | : | | : : || | : : | | : || | : : : : || |
Db      296 VNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTVLWRYTGT---RPSNLAKNT 351
Qy      347 KIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKF 406
      : | || | : || | | | : || | : | | | : || | : | | :
Db      352 ILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMMPLFGDQMDNAKRMETRGA 411
Qy      407 GVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTG 466
      || : : : : | : | : | : : | | : | : | | : : : :
Db      412 GVTLVNLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAVFWVEYVMRHK 471
Qy      467 GATHLKPYPVFQQPWHEQYLFDFVFLGLTLGLTLWL-----CGKLLGMAVWWLARGAR 518
      || || : | : : || || : | : : | | | |
Db      472 GAPHLRPAHDLTWYQYHSLDVGFLLAIVLTVVFIVYKSCAYGCRKCFG-----GKG 524
Qy      519 KVKET 523
      : || :
Db      525 RVKKS 529

```

RESULT 10

JN0619

glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human

N;Alternate names: UDP-glucuronosyltransferase 2B-11

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000

C;Accession: JN0619; A27878

R;Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.

Biochem. Biophys. Res. Commun. 194, 496-503, 1993

A;Title: cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase 2B subfamily.

A;Reference number: JN0619; MUID:93326164; PMID:8333863

A;Accession: JN0619

A;Molecule type: mRNA

A;Residues: 1-528 <JIN>

A;Cross-references: GB:AF081793; NID:g3426331

A;Experimental source: liver

R;Jackson, M.R.; McCarthy, L.R.; Harding, D.; Wilson, S.; Coughtrie, M.W.H.; Burchell, B.

Biochem. J. 242, 581-588, 1987

A;Title: Cloning of a human liver microsomal UDP-glucuronosyltransferase cDNA.

A;Reference number: A27878; MUID:87241362; PMID:3109396
 A;Accession: A27878
 A;Molecule type: mRNA
 A;Residues: 1-108,'F',110-170,'RP',173-381,'K',383-384,'SPR',388-395,'F',397-528
 <JAC>
 A;Cross-references: GB:Y00317; NID:g37588; PIDN:CAA68415.1; PID:g37589
 C;Genetics:
 A;Gene: GDB:UGT2B4; UGT2B11
 A;Cross-references: GDB:5891331; OMIM:600067
 A;Map position: 4q13-4q13
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-528/Product: glucuronosyltransferase 2B-11 #status predicted <MET>
 F;492-509/Domain: transmembrane #status predicted <TMM>
 F;315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.7%; Score 656.5; DB 2; Length 528;
 Best Local Similarity 33.9%; Pred. No. 1.6e-43;
 Matches 173; Conservative 85; Mismatches 213; Indels 39; Gaps 15;

Qy	34	SHYLLMDRVSQILQDHGHNVTMLNHKRG----	PFMPDFKKEEKSYQVISWLAPEDHQREF	89
		: : : :	: : :	
Db	34	SHWMNIKTILDELVQRGHEVTVLASSASISFDPN	SPSTLKFEVYPVSLTKTEFEDIKQL	93
Qy	90	-----KKSFDFFLEETLGGRGKFENLLNVLEYL	ALQCSHFLNRKDIMDSLKNENFDM	141
		: : : :	: : : :	
Db	94	VKRWAELPKDTFWSYLSQVQEIMWTFNDILRK	F-----CKDIVSNKKLMKKLQESRFDV	147
Qy	142	VIVETFDYCPF--LIAEKLKGFVAILSTSFG-SLE--	FGLPIPLSYVPVFRSLLTDHM	195
		: : : :		
Db	148	VLADA--VFPFGELLAELLKIPFVYSLRFSPGYA	IEKHSGGLLFPPSYVPVVMSELSQDM	205
Qy	196	DFWGRVKN--FLMFFSFCRRQQHMQSTFDNTI	KEHFTEGSRPVLSHLLLKAEWFINSDF	253
		: : : : :	: : : :	
Db	206	TFIERVKNMIVLYFEFWQIFDMKK-WDQFYSE--	VLGRPTTLSETMAKADIWLIRNYW	262
Qy	254	AFDFARPLLNTVYVGGLMEKPIKPVPQDLENF	IAKFGDSGFVLVTLGSMV-NTCQNPEI	312
		: : :	: : :	
Db	263	DFQFPHPLLPNVEFVGGLHCKPAKPLPKEMEE	FVQSSGENGVVVFSLGSMVSNTSE--ER	320
Qy	313	FKEMNNAFAHLPQGVWKCQCSHWPKDVHLAAN	VKIVDWLPQSDLLAHPSIRLFVTHGGQ	372
		: : : : : :	: : :	
Db	321	ANVIASALAKIPQKVLWRFDGN---KPD	TGLNTRLYKWIPQNDLLGHPKTRAFITHGGA	377
Qy	373	NSIMEAIQHGVPVMVGIPFLFGDQPENMVR	VEAKKFGVSIQLKKLKAETLALKMKQIMEDKR	432
		: :	: : : :	
Db	378	NGIYEAIYHGIPMVGVPDLLADQPDNIAH	MKAKGAAVSLDFHTMSSTDLLNALKTVINDPL	437
Qy	433	YKSAAVAASVILRSHPLSPTQRLVGWIDHVL	QTGGATHLKPYVFQQPWHEQYLFDFVFVFL	492
		: : :	: : : :	
Db	438	YKENAMKLSRIHHDQPVKPLDRAVFWIEF	VMRHKGAKHLRVAHDLTWFQYHSLDVTGFL	497
Qy	493	LGLTLGTLWLCGKLLGMVAV-WLRGARKVK		521
		: : : :		
Db	498	LACVATVIFIITKCL-FCVWKFEVRTGKKGK		526

RESULT 11

A35366

glucuronosyltransferase (EC 2.4.1.17) UDPGTh-2 precursor - human

C;Species: Homo sapiens (man)

C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 29-Sep-1999

C;Accession: A35366

R;Ritter, J.K.; Sheen, Y.Y.; Owens, I.S.

J. Biol. Chem. 265, 7900-7906, 1990

A;Title: Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 cells. 3,4-Catechol estrogens and estriol as primary substrates.

A;Reference number: A35366; MUID:90243659; PMID:2159463

A;Accession: A35366

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-529 <RIT>

A;Cross-references: GB:J05428; NID:g340079; PIDN:AAA36793.1; PID:g340080

C;Genetics:

A;Gene: GDB:UGT2B7; UGT2B9

A;Cross-references: GDB:5892203; OMIM:600218

A;Map position: 4q13-4q13

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 23.6%; Score 654.5; DB 2; Length 529;
Best Local Similarity 31.5%; Pred. No. 2.3e-43;
Matches 163; Conservative 88; Mismatches 212; Indels 55; Gaps 14;

```

Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRG-PFMPD-----FKKEEKSYSY---Q 75
      ||:: : : | || ||:| | : | |::: |
Db      34 SHWMNIKTILDELIQRGHEVTVLASSASILFDPNNSSALKIEIYPTSLTKTELENFIMQQ 93

Qy      76 VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYIALQ-CSHFLNRKDIMDS 133
      : | |:| :| : : : :::: : : | :: | |
Db      94 IKRWSDLPKD-----TFWLYFSQV-----QEIMSIFGDITRKFCCKDVVSNNKKFMKK 139

Qy     134 LKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTS----FGSLEFGLPIPLSYVPVFRS 189
      :: ||:: : | |:|| || || | | | | | |
Db     140 VQESRFDVIFADAIFPCSELLAELENIPFVYSLSFSPGYTFEKHSGGFIFPPSYVPVMS 199

Qy     190 LLTDHMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTE---GSRPVLSHLLLKA 244
      ||| | | |||| ::::| | | | : | | | : ||
Db     200 ELTDQMTFMERVKNMIIYVLYFDF-----WFEIFDMKKWDQFYSEVLGRPTTLSETMGKA 253

Qy     245 ELWFINSDFAFDFARPLLPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV 304
      ::| | : : | | |||| :||| || ||:::|::: |::| | : ||||
Db     254 DVWLIRNSWNFQFPHPLLPNVDFVGGLHCKPAKPLPKEMEDFVQSSGENGVVVFSLGSMV 313

Qy     305 NTCQNPEIFKEMNNAFAHLPPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsir 364
      : | : :| | :|| |:| : | | | :| :||:| || |
Db     314 SN-MTEERANVIASALAIQIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTR 369

Qy     365 LFVTHGGQNSIMEAIQHGVPMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM 424
      |:|||| | | ||| ||:||||||| ||::: :::: | : : : | :
Db     370 AFITHGGANGIYEAIYHGIPMVGIPLFADQPDNIAHMKARGAAVRVDFNTMSSTDLLNAL 429

```

Qy 425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQY 484
 |::: | || : | | | : | | | |:: |:: || |:: | : :
 Db 430 KRVINDPSYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHADLTWFQYH 489
 Qy 485 LFDVVFVLLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
 || ||| ::: | | : ||| |:
 Db 490 SLDVIGFLLVCVATVIFIVTKCCLEFCFW--KFARKAKK 525

RESULT 12

S15089

glucuronosyltransferase (EC 2.4.1.17) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C;Accession: S15089

R;Lazard, D.; Zupko, K.; Poria, Y.; Nef, P.; Lazarovits, J.; Horn, S.; Khen, M.; Lancet, D.

Nature 349, 790-793, 1991

A;Title: Odorant signal termination by olfactory UDP glucuronosyl transferase.

A;Reference number: S15089; MUID:91156050; PMID:1900353

A;Accession: S15089

A;Molecule type: mRNA

A;Residues: 1-527 <LAZ>

A;Cross-references: GB:X57565; NID:g57762; PIDN:CAA40797.1; PID:g3980217

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.5%; Score 650; DB 2; Length 527;
 Best Local Similarity 31.2%; Pred. No. 5.2e-43;
 Matches 166; Conservative 87; Mismatches 205; Indels 74; Gaps 12;

Qy 7 LLLVGFLLP GVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP- 65
 | |:: | | | : | : ||:: | : : | | |:: | |:
 Db 12 LSLLGMSLGGNVL-----IWPMEGSHWLNVKIIDE LLRKEHNVTVLVASGALFITP 63
 Qy 66 -----DFKKEE-----KSYQVISWL----APEDHQREFKKSFDFFLEETLGG 103
 | ||: | : |::|| : | : |:: | |
 Db 64 SVSPSLTFEIIYPVPFPGKEKIESVIKDF-VLTWLENRSPSTIWTIFYKEMAKVIEEFHLVS 122
 Qy 104 RGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFPV 163
 || | | : : | | : |::: : | : | || | |:
 Db 123 RG-----ICDGVLKNEKLMTKLQRGKFEVLLSDPVFPFCGDIVALKLGIPFI 168
 Qy 164 AILSTSFSGSLEFG-----LPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCR 212
 || | : | || | | || | | | | |:: | : : |
 Db 169 Y-----SLRFSPASTVEKHCGKVPFPSPSYVPAILSELTDQMSFADRVRNFISY----R 217
 Qy 213 RQOHMQSTFDNTIKEHFTE--GSRPVLSHLLLKAELWFINSDFAFDFARPLLPTVYVGG 270
 | : | | ::: | | : ||:: | : : | : | || | | : ||
 Db 218 MQDYMFETLWKQWDSYYSKALGRPTTLCETMGKAEIWLRTYWDFFPRPYLPNFEEVVG 277
 Qy 271 LMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIVK 330
 | || |:: |:: | | : | | : |:: | | : | | |:: |:
 Db 278 LHCKPAKPLPKEME EFVQTSGEHG VVVFSLGSMVKNL-TEEKANLIASALAQIPQKVLR 336
 Qy 331 CQCSHWPKDVH LAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVP MVGIPL 390
 : | : | : : |:: |:: | | | |:: | | | | |:: |:: |:

Db 337 YK---GKIPATLGSNTRLFDWIPQNDLLGHPKTRAFITHGGTNGIYEAIYHGIPMVGVP 393

Qy 391 FGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLS 450
| |||:|: ::|| | : : : : | : : : : || |: | | |:

Db 394 FADQPDNIAHMKAKGAAVEVNMNMTSADLLSAVRVINEPFYKENAMRLSRIHHDQPVK 453

Qy 451 PTQRLVGWIDHVLQTTGGATHLKPYPVFPQWHEQYLFDFVFLGLTLGLTLWL 502
| | | ||: |: : || ||: | : : || ||| : |

Db 454 PLDRAVFWIEFVMRHKGAKHLRVAHDLSWFQYHSLDVIGFLLACMASAILL 505

RESULT 13

A48633

glucuronosyltransferase (EC 2.4.1.17) precursor - human

N;Alternate names: dihydrotestosterone/androstanediol UDP-

glucuronosyltransferase isoform 3, udpgth-3; UDP glucuronosyltransferase 2 family, protein B15

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999

C;Accession: A48633; I38559

R;Chen, F.; Ritter, J.K.; Wang, M.G.; McBride, O.W.; Lubet, R.A.; Owens, I.S. Biochemistry 32, 10648-10657, 1993

A;Title: Characterization of a cloned human dihydrotestosterone/androstanediol UDP-glucuronosyltransferase and its comparison to other steroid isoforms.

A;Reference number: A48633; MUID:94002056; PMID:8399210

A;Accession: A48633

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-530 <CHE>

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIP:138786)

R;Green, M.D.; Oturu, E.M.; Tephly, T.R.

Drug Metab. Dispos. 22, 799-805, 1994

A;Title: Stable expression of a human liver UDP-glucuronosyltransferase (UGT2B15) with activity toward steroid and xenobiotic substrates.

A;Reference number: I38559; MUID:95136867; PMID:7835232

A;Accession: I38559

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-530 <RES>

A;Cross-references: EMBL:U08854; NID:g475758; PIDN:AAC50077.1; PID:g475759

C;Genetics:

A;Gene: GDB:UGT2B15; UGT2B8

A;Cross-references: GDB:5892418; OMIM:600219

A;Map position: 4q13-4q13

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.4%; Score 649; DB 2; Length 530;

Best Local Similarity 31.8%; Pred. No. 6.3e-43;

Matches 155; Conservative 90; Mismatches 218; Indels 24; Gaps 10;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVI-SWLAPEDHQREFKKS 92

||:| : : | || ||:| : | : | | : |

Db 34 SHWINMKTILEELVQRGHEVTVLTSASTLVNASKSSAIKLEVYPTSLTKNDLEDSLLKI 93

Qy 93 FDFFLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMVIV 144

```

      | ::      : | : : | : | :      | : | : | | : | ::::
Db      94 LDRWIYGV--SKNTFWSYFSQLQELCWEYYDYSNKLCKDAVLNKKLMMKLQESKFDVILA 151

Qy      145 ETFDYCPFLIAEKLGPFPVAILSTSEFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWGR 200
      : : | | : | | | : | | | | | | | : | | | |
Db      152 DALNPCGELLAELFNIPFLYSLRFSVGYTFEKNNGGGLFPSPSYVPVVMSELSQDMIFMER 211

Qy      201 VKNF--LMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDFA 258
      : | | : : | | : : : | | | | : | | : | : | : |
Db      212 IKNMIHMLYFDFWFQIYDLKK-WDQFYSE--VLGRPTTLFETMGKAEMWLIRTYWDFEFP 268

Qy      259 RPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN 318
      | | | | : | | | | | | : | : | : | : | : | : | : |
Db      269 RPFLPNVDFVGGHLCKPAKPLPKEMEETFVQSSGENGIVVFSLGSMISN-MSEESANMIAS 327

Qy      319 AFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEA 378
      | | : | | : | : | | : | : | | | : | | | | | | |
Db      328 ALAQIPQKVLWRFD---GKKPNTLGSNTRLYKWLQPNDLLGHPKTKAFITHGGTNGIYEA 384

Qy      379 IQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAV 438
      | | : | | | | | | | | : | : : | : : : : | : | : | | :
Db      385 IYHGIPMVGIPLFADQHDNIAHMKAKGAALSVDIRTSSRDLLNALKSVINDPVYKENVM 444

Qy      439 AASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFLGLTLG 498
      | | : | | | | | : : | | : | : : | : : | | |
Db      445 KLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWQYHSLDVIAFLACVAT 504

Qy      499 TLWLCGK 505
      : : : |
Db      505 VIFIITK 511

```

RESULT 14

JN0620

UDP-glucuronosyltransferase (EC 2.4.1.-) 2B-10 precursor - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999

C;Accession: JN0620

R;Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.

Biochem. Biophys. Res. Commun. 194, 496-503, 1993

A;Title: cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase 2B subfamily.

A;Reference number: JN0619; MUID:93326164; PMID:8333863

A;Accession: JN0620

A;Molecule type: mRNA

A;Residues: 1-528 <JIN>

A;Cross-references: GB:X63359; NID:g516149; PIDN:CAA44961.1; PID:g516150

A;Experimental source: liver

C;Superfamily: glucuronosyltransferase

C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-528/Product: UDP-glucuronosyltransferase 2B-10 #status predicted <MET>

F;491-508/Domain: transmembrane #status predicted <TMM>

F;66,314,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

23.2%; Score 642; DB 2; Length 528;

Best Local Similarity 31.6%; Pred. No. 2.2e-42;
Matches 167; Conservative 82; Mismatches 213; Indels 66; Gaps 13;

```

Qy      31 VGGSHYLLMDRVSQILQD---HGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQR 87
      | : | | : |:: | |::| | : : | |
Db      27 VWAAEYSLWMNMKTILKELVQRGHEVTVL-----ASSASIL--FDPNDSST 70

Qy      88 EFKKSFDFLFLEETLGGRGKFENLLNVL-----EYLALQ 120
      : : | : | : |:: | : :
Db      71 LKLEVYPTSLTKT-----EFENIIMQLVKRLSEIQKDTFWLPFSQEQEILWAINDIIRNF 125

Qy     121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFG-SLE---FG 176
      | : : | : | | : |::| : : | |::| | | | | | |
Db     126 CKDVVSNKKLMKKLQESRFDIVFADAYLPCGELLAELFNIPFVYSHSFSPGYSFERHSGG 185

Qy     177 LPIPLSYVPVFRSLLTDHMDFWGRVKN--FLMFFSFCCRQOQHMOSTFDNTIKEHFTEGSR 234
      | | | | | | | : | | | | | | : : : | | : : | : | |
Db     186 FIFPPSYVPVVMKSLSDQMTFMERVKNMPLYVLYFDFWFQIFNMKK-WDQFYSE--VLGRP 242

Qy     235 PVLSHLLKLAELWFINSDFAFDFARPLLPTVYVGGLMKPKPKVPQDLENFIAKFGDSG 294
      | | : |::| : : : | | | | | : | | | | | | : | : |
Db     243 TTLSETMRKADIWLMRNSWNFKFPHPLPNVDFVGGHLHCKPAKPLPKEMEEFVQSSGENG 302

Qy     295 FVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANKIVDWLPQ 354
      | : : | | | : | : | : | | : | : | : | : | : |
Db     303 VVVFSLGSMVSN-MTEERANVIATALAKIPQKVLWRFDGN---KPDALGLNTRLYKWIPQ 358

Qy     355 SDLLAHPsirLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKK 414
      : | | | | | | | : | | | | | | | | | : | : | : |
Db     359 NDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGIPLFQDQPDNIAHMKAKGA AVRVDENT 418

Qy     415 LKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLPKY 474
      : : | : : | | : | | : | | | | : : | : : | | :
Db     419 MSSTDLLNALKTVINDPYKENIMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA 478

Qy     475 VFQQPWHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
      | : : | | | | : : | | : | | :
Db     479 AHNLTWFQYHSLDVIGFLLACVATVLFIIITKCCLFCFW--KFARKGKK 524

```

RESULT 15

S07390

glucuronosyltransferase (EC 2.4.1.17) 3 precursor - rat

N;Alternate names: 17beta-hydroxysteroid UDP-glucuronosyltransferase; UDP-glucuronosyltransferase isoform 50K

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999

C;Accession: S07390; A33236; A28460; S59626

R;Harding, D.; Wilson, S.M.; Jackson, M.R.; Burchell, B.; Green, M.D.; Tephly, T.R.

Nucleic Acids Res. 15, 3936, 1987

A;Title: Nucleotide and deduced amino acid sequence of rat liver 17beta--hydroxysteroid UDP-glucuronosyltransferase.

A;Reference number: S07390; MUID:87231096; PMID:3108864

A;Accession: S07390

A;Molecule type: mRNA

A;Residues: 1-530 <HAR>

A;Cross-references: EMBL:Y00156
 A;Experimental source: liver
 A;Accession: A33236
 A;Molecule type: protein
 A;Residues: 24-61 <HAR2>
 A;Experimental source: liver
 R;Mackenzie, P.I.
 J. Biol. Chem. 262, 9744-9749, 1987
 A;Title: Rat liver UDP-glucuronosyltransferase. Identification of cDNAs encoding two enzymes which glucuronidate testosterone, dihydrotestosterone, and beta-estradiol.
 A;Reference number: A28460; MUID:87250645; PMID:3110162
 A;Accession: A28460
 A;Molecule type: mRNA
 A;Residues: 1-118,'G',120-240,'L',242-423,'S',425-499,'T',501-530 <MAC>
 A;Experimental source: liver
 R;Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugiura, T.; Waku, K.
 Biochem. J. 312, 301-308, 1995
 A;Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of rat liver: their effect on enzyme activity.
 A;Reference number: S59626; MUID:96077159; PMID:7492328
 A;Accession: S59626
 A;Molecule type: protein
 A;Residues: 24-44 <YAM>
 A;Experimental source: liver
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-530/Product: glucuronosyltransferase #status experimental <MAT>
 F;494-510/Domain: transmembrane #status predicted <TMM>

Query Match 23.1%; Score 640; DB 2; Length 530;
 Best Local Similarity 34.2%; Pred. No. 3.2e-42;
 Matches 167; Conservative 81; Mismatches 189; Indels 52; Gaps 15;

Qy	34	SHYLLMDRVSQILQDHGHNV-----MLNHKRGPFMPDFKKEEKSYQVISWLPAPEDH	85
		: : : : : : : :	
Db	34	SHWMNIKTILDELVQRGHEVTVLKPSAYYVLDPKKS---PDLKFETFTSV----SKDEL	86
Qy	86	QREFKKSFDFFLEE-----TLGGRGKFENLLNVLE--YLALQCSHF LN RKD IMDSLKNEN	138
		: : : : : : : :	
Db	87	ENYFIKLVDVWTYELQRDTCLSYSPLLQNMIDEFSDYYLSL-CKDTVSNKQLMAKLQESK	145
Qy	139	FDMVIVETFDYCPFLIAEKLKGFVAILSTSFSG-----SLEFGLPIPLSYVPVFRSLIT	192
		: : : : :	
Db	146	FDVLLSDPVAACGELIAEVLHIPFLYSLRFSPGYKIEKSSGRFIL--PPSYVPVILSGMG	203
Qy	193	DHMDFWGRVKNFL--MFFSFCRRQOHM--QSTFDNTIKEHFTEGSRPVLSHLLLKAE LWF	248
		: : : : : : :	
Db	204	GPMTFIDRVKNMICTLYFDF--WFHMFNAKKWDPFYSEIF--GRPTTLAETMGKAEMWL	258
Qy	249	INSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQ	308
		: : : : : : : : :	
Db	259	IRSYWDLEFPHPPTLPNVVDYIGGLQCRPPKPLPKDMEFVQSSGEHGVVVFSLGSMVSS--	316
Qy	309	NPEIFKEMNN---AFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIR	364
		: : : : : : : :	

Db 317 ---MTEEKANAIAWALAQIPQKVLWKFD---GKTPATLGPNTRVYKWLPQNDLLGHPKTK 370
 Qy 365 LFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM 424
 ||||| | : ||| ||:|||||:|:| :|: : || |:: :: : | :
 Db 371 AFVTHGGANGVYEAIYHGIPMVGIPMFGEQHDNIAHMAVAKGAAVTLNIRTMSKTDLENAL 430
 Qy 425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPWHEQY 484
 |:|: : || || | | |: | : | |: |: : || ||:| |:: :
 Db 431 KEIINNPFYKKNVWLSTIHHDQPMKPLDKAVFWIEFVMRHKGAKHLRPLGHDLPWYQYH 490
 Qy 485 LFDVVFVLL 493
 || |||
 Db 491 SLDVIGFLL 499

Search completed: May 7, 2004, 17:33:21
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 17:31:25 ; Search time 48 Seconds
(without alignments)
3024.321 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						

1	2768	100.0	523	10	US-09-946-374-282	Sequence 282, App
2	2768	100.0	523	12	US-10-006-485A-282	Sequence 282, App
3	2768	100.0	523	12	US-10-013-907A-282	Sequence 282, App
4	2768	100.0	523	12	US-10-015-499A-282	Sequence 282, App
5	2768	100.0	523	12	US-10-013-910A-282	Sequence 282, App
6	2768	100.0	523	12	US-10-226-254A-282	Sequence 282, App
7	2768	100.0	523	12	US-10-015-395A-282	Sequence 282, App
8	2768	100.0	523	14	US-10-006-856A-282	Sequence 282, App
9	2768	100.0	523	14	US-10-006-818A-282	Sequence 282, App
10	2768	100.0	523	14	US-10-015-393A-282	Sequence 282, App
11	2768	100.0	523	14	US-10-015-869A-282	Sequence 282, App
12	2768	100.0	523	14	US-10-012-121A-282	Sequence 282, App
13	2768	100.0	523	14	US-10-006-116A-282	Sequence 282, App
14	2768	100.0	523	14	US-10-006-117A-282	Sequence 282, App
15	2768	100.0	523	14	US-10-017-527A-282	Sequence 282, App
16	2768	100.0	523	14	US-10-013-913A-282	Sequence 282, App
17	2768	100.0	523	14	US-10-007-194A-282	Sequence 282, App
18	2768	100.0	523	14	US-10-013-430A-282	Sequence 282, App
19	2768	100.0	523	14	US-10-011-671A-282	Sequence 282, App
20	2768	100.0	523	14	US-10-012-755A-282	Sequence 282, App
21	2768	100.0	523	14	US-10-015-386A-282	Sequence 282, App
22	2768	100.0	523	14	US-10-011-692A-282	Sequence 282, App
23	2768	100.0	523	14	US-10-006-768A-282	Sequence 282, App
24	2768	100.0	523	14	US-10-017-610A-282	Sequence 282, App
25	2768	100.0	523	14	US-10-006-063A-282	Sequence 282, App
26	2768	100.0	523	14	US-10-020-063A-282	Sequence 282, App
27	2768	100.0	523	14	US-10-015-391A-282	Sequence 282, App
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29	2768	100.0	523	14	US-10-011-833A-282	Sequence 282, App
30	2768	100.0	523	14	US-10-006-041A-282	Sequence 282, App
31	2768	100.0	523	14	US-10-015-822A-282	Sequence 282, App
32	2768	100.0	523	14	US-10-015-387A-282	Sequence 282, App
33	2768	100.0	523	14	US-10-006-130A-282	Sequence 282, App
34	2768	100.0	523	14	US-10-006-172A-282	Sequence 282, App
35	2768	100.0	523	14	US-10-017-253A-282	Sequence 282, App
36	2768	100.0	523	14	US-10-015-392A-282	Sequence 282, App
37	2768	100.0	523	14	US-10-017-306A-282	Sequence 282, App
38	2768	100.0	523	14	US-10-017-867A-282	Sequence 282, App
39	2768	100.0	523	14	US-10-012-064A-282	Sequence 282, App
40	2768	100.0	523	14	US-10-013-909A-282	Sequence 282, App
41	2768	100.0	523	14	US-10-015-671A-282	Sequence 282, App
42	2768	100.0	523	14	US-10-015-610A-282	Sequence 282, App
43	2768	100.0	523	14	US-10-012-137A-282	Sequence 282, App
44	2768	100.0	523	14	US-10-012-752A-282	Sequence 282, App
45	2768	100.0	523	14	US-10-012-754A-282	Sequence 282, App

ALIGNMENTS

RESULT 1
 US-09-946-374-282
 ; Sequence 282, Application US/09946374
 ; Publication No. US20030073129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
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Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
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Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
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Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
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Db    181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
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Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360
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Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
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Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
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Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480
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 Qy 481 HEQYLFDFVFVLLGLTLGTLWLCLCGKLLGMAVWWLRGARKVKET 523
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 Db 481 HEQYLFDFVFVLLGLTLGTLWLCLCGKLLGMAVWWLRGARKVKET 523

RESULT 2

US-10-006-485A-282

; Sequence 282, Application US/10006485A
 ; Publication No. US20030064062A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan l.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C9
 ; CURRENT APPLICATION NUMBER: US/10/006,485A
 ; CURRENT FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: 60/098716
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098723
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098749
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 ; PRIOR FILING DATE: 1998-09-01
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 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/099536
 ; PRIOR FILING DATE: 1998-09-09
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 ; PRIOR APPLICATION NUMBER: 60/099598
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 ; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-10-07
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Qy 181 LSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
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 Db 181 LSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
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 Db 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCShWPKDVHLAANVKIVDWLPQSDLLAH 360
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Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPW 480
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Qy 481 HEQYLFDFVFLGLTLGLTLWLCLCGKLLGMAVWWLRGARKVKET 523
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RESULT 3

US-10-013-907A-282

; Sequence 282, Application US/10013907A

; Publication No. US20030064925A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C34

; CURRENT APPLICATION NUMBER: US/10/013,907A

; CURRENT FILING DATE: 2001-12-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 282

; LENGTH: 523

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-013-907A-282

Query Match 100.0%; Score 2768; DB 12; Length 523;
 Best Local Similarity 100.0%; Pred. No. 6.6e-272;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
        |
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60

Qy     61 GPFMPDFKKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |
Db     61 GPFMPDFKKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFGSLEFGLPIP 180
        |
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
        |
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
        |
Db    241 LLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
        |
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPVVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
        |
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPVVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480
        |
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480

Qy    481 HEQYLFDFVVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
        |
Db    481 HEQYLFDFVVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
  
```

RESULT 4

US-10-015-499A-282

; Sequence 282, Application US/10015499A

; Publication No. US20030065142A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-499A-282

```

```

Query Match          100.0%; Score 2768; DB 12; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNV'TMLNHKR 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNV'TMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILST'SFGSLEFGLPIP 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILST'SFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLENTVYVGGIMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LLKAELWFINSDFAFDFARPLLENTVYVGGIMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC'SHWPKDVH'LAANVKIVDWLPQSDLLAH 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC'SHWPKDVH'LAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIP'LFQDQ'PENMVRVEAKKFGVSIQLKKLKAETL 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIP'LFQDQ'PENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQ'TGGATHL'KPYVFQ'QPW 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQ'TGGATHL'KPYVFQ'QPW 480

Qy    481 HEQYLF'DV'FV'FLLGLTLGTLWLCGKLLGMAV'VW'LRGARKVKET 523
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 HEQYLF'DV'FV'FLLGLTLGTLWLCGKLLGMAV'VW'LRGARKVKET 523

```

RESULT 5

US-10-013-910A-282

; Sequence 282, Application US/10013910A
; Publication No. US20030187192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C33
; CURRENT APPLICATION NUMBER: US/10/013,910A
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-910A-282

Query Match 100.0%; Score 2768; DB 12; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Qy	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Qy	481	HEQYLFDFVFVLLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVFVLLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET	523

RESULT 6

US-10-226-254A-282

; Sequence 282, Application US/10226254A

; Publication No. US20030224478A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```

; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE:  P2830P1C68
; CURRENT APPLICATION NUMBER:  US/10/226,254A
; CURRENT FILING DATE:  2002-08-21
; PRIOR APPLICATION NUMBER:  60/098716
; PRIOR FILING DATE:  1998-09-01
; PRIOR APPLICATION NUMBER:  60/098723
; PRIOR FILING DATE:  1998-09-01
; PRIOR APPLICATION NUMBER:  60/098749
; PRIOR FILING DATE:  1998-09-01
; PRIOR APPLICATION NUMBER:  60/098750
; PRIOR FILING DATE:  1998-09-01
; PRIOR APPLICATION NUMBER:  60/098803
; PRIOR FILING DATE:  1998-09-02
; PRIOR APPLICATION NUMBER:  60/098821
; PRIOR FILING DATE:  1998-09-02
; PRIOR APPLICATION NUMBER:  60/098843
; PRIOR FILING DATE:  1998-09-02
; PRIOR APPLICATION NUMBER:  60/099536
; PRIOR FILING DATE:  1998-09-09
; PRIOR APPLICATION NUMBER:  60/099596
; PRIOR FILING DATE:  1998-09-09
; PRIOR APPLICATION NUMBER:  60/099598
; PRIOR FILING DATE:  1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-254A-282

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Query Match          100.0%;  Score 2768;  DB 12;  Length 523;
Best Local Similarity 100.0%;  Pred. No. 6.6e-272;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
        |||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60

Qy      61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        |||
Db      61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy      121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAILSTSFGSLEFGLPIP 180
        |||
Db      121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAILSTSFGSLEFGLPIP 180

Qy      181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
        |||
Db      181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy      241 LLKAELWFINSDFAFDFAFARPLLNPNTVYVGGLMKPIKVPQDLENFIAKFGDSGFVLVTL 300
        |||
Db      241 LLKAELWFINSDFAFDFAFARPLLNPNTVYVGGLMKPIKVPQDLENFIAKFGDSGFVLVTL 300

Qy      301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

```

```

Db      301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCSEHWPKDVHLAANVKIVDWLPQSDLLAH 360
Qy      361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
Db      361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
Qy      421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480
Db      421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW 480
Qy      481 HEQYLFDFVFVFLGLTLGTLWLCLCGKLLGMAVWWLRGARKVKET 523
Db      481 HEQYLFDFVFVFLGLTLGTLWLCLCGKLLGMAVWWLRGARKVKET 523

```

RESULT 7

US-10-015-395A-282

```

; Sequence 282, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-395A-282

```

```

Query Match      100.0%; Score 2768; DB 12; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHHR 60
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHHR 60
Qy      61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

```

Db	61	GPFPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Qy	481	HEQYLFDFVVFLLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVVFLLGLTLGTLWLCLGKLLGMAVWWLRGARKVKET	523

RESULT 8

US-10-006-856A-282

; Sequence 282, Application US/10006856A

; Publication No. US20030044841A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C14

; CURRENT APPLICATION NUMBER: US/10/006,856A

; CURRENT FILING DATE: 2002-05-10

; NUMBER OF SEQ ID NOS: 477

; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C4
 ; CURRENT APPLICATION NUMBER: US/10/006,818A
 ; CURRENT FILING DATE: 2001-12-06
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 282
 ; LENGTH: 523
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-006-818A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;
 Best Local Similarity 100.0%; Pred. No. 6.6e-272;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Db	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Qy	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Db	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480

Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy 481 HEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523
 |||

Db 481 HEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523

RESULT 10

US-10-015-393A-282

; Sequence 282, Application US/10015393A
 ; Publication No. US20030069179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C46
 ; CURRENT APPLICATION NUMBER: US/10/015,393A
 ; CURRENT FILING DATE: 2002-06-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 282
 ; LENGTH: 523
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-015-393A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;
 Best Local Similarity 100.0%; Pred. No. 6.6e-272;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
 |||

Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
 |||

Db 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180
 |||

Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIP 180

Qy 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHL 240
 |||

Db 181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
 Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
 Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 GSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360
 Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
 Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480
 Qy 481 HEQYLFVDVVFLLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 HEQYLFVDVVFLLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523

RESULT 11

US-10-015-869A-282

; Sequence 282, Application US/10015869A

; Publication No. US20030073130A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin I.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C45

; CURRENT APPLICATION NUMBER: US/10/015,869A

; CURRENT FILING DATE: 2002-06-25

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 282

; LENGTH: 523

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-015-869A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;

Best Local Similarity 100.0%; Pred. No. 6.6e-272;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
      |||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      |||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
      |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
      |||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFAFARPLLNTVYVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300
      |||
Db    241 LLKAELWFINSDFAFDFAFARPLLNTVYVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300

Qy   301 GSMVNTCQNPEIFKEMNNAFAHLPOGVIWKCQCShWPKDVHLaANVKIVDWLPQSDLLAH 360
      |||
Db   301 GSMVNTCQNPEIFKEMNNAFAHLPOGVIWKCQCShWPKDVHLaANVKIVDWLPQSDLLAH 360

Qy   361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
      |||
Db   361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy   421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
      |||
Db   421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy   481 HEQYLFDFVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523
      |||
Db   481 HEQYLFDFVFVLLGLTLGTLWLWLCGKLLGMAVWWLRGARKVKET 523

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RESULT 12

US-10-012-121A-282

; Sequence 282, Application US/10012121A

; Publication No. US20030073810A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

```
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 282
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-121A-282
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Query Match          100.0%; Score 2768; DB 14; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHRK 60
      |||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHRK 60

Qy     61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      |||
Db     61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP 180
      |||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
      |||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300
      |||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360
      |||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
      |||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
      |||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
      |||
Db    481 HEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
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RESULT 13
US-10-006-116A-282
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; Sequence 282, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812

; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
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; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
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; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-30
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; PRIOR APPLICATION NUMBER: 60/102570
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; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
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; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679


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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
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Query Match          100.0%; Score 2768; DB 14; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
          |
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60

Qy     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
          |
Db     61 GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP 180
          |
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
          |
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
          |
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
          |
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
```

Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLGDPENMVRVEAKKFGVSIQLKKLKAETL 420
 |||
 Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLGDPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480
 |||
 Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW 480

Qy 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
 |||
 Db 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 14

US-10-006-117A-282

; Sequence 282, Application US/10006117A

; Publication No. US20030082627A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C13

; CURRENT APPLICATION NUMBER: US/10/006,117A

; CURRENT FILING DATE: 2002-03-19

; Prior Application removed - See File Wrapper or Palm

; PRIOR FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 282

; LENGTH: 523

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-006-117A-282

Query Match 100.0%; Score 2768; DB 14; Length 523;

Best Local Similarity 100.0%; Pred. No. 6.6e-272;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
 |||

Db 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
 |||

Db	61	GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVAILSTSFGSLEFGLPIP	180
Qy	181	LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPW	480
Qy	481	HEQYLFDFVVFLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523
Db	481	HEQYLFDFVVFLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET	523

RESULT 15

US-10-017-527A-282

; Sequence 282, Application US/10017527A

; Publication No. US20030082628A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C63

; CURRENT APPLICATION NUMBER: US/10/017,527A

; CURRENT FILING DATE: 2001-12-13

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
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; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 2768; DB 14; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.6e-272;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP 180

Qy    181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy    481 HEQYLFDFVFVFLGLTLGLTLWLCCGKLLGMAVWWLRGARKVKET 523
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 HEQYLFDFVFVFLGLTLGLTLWLCCGKLLGMAVWWLRGARKVKET 523
```

Search completed: May 7, 2004, 17:34:58
Job time : 50 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:28:39 ; Search time 45 Seconds
(without alignments)
3667.023 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWVWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1	2754	99.5	523	4	Q8NBP2	Q8nbp2 homo sapien
2	2193	79.2	523	4	Q96DM6	Q96dm6 homo sapien
3	1815	65.6	523	11	Q8R0Y5	Q8r0y5 mus musculu
4	1804	65.2	523	11	Q8JZZ0	Q8jzz0 mus musculu
5	1802	65.1	523	11	Q8VC11	Q8vc11 mus musculu
6	963	34.8	221	4	Q8NAW4	Q8naw4 homo sapien
7	914.5	33.0	252	4	Q8IYS9	Q8iys9 homo sapien
8	792	28.6	302	11	Q8BRY7	Q8bry7 mus musculu
9	727	26.3	541	13	Q98TB5	Q98tb5 gallus gall
10	698	25.2	541	11	Q91W57	Q91w57 mus musculu
11	689.5	24.9	529	6	Q9TSL6	Q9tsl6 macaca fasc
12	685.5	24.8	529	6	O97951	O97951 macaca fasc
13	685.5	24.8	534	11	Q8BWQ1	Q8bwq1 mus musculu
14	684.5	24.7	498	6	Q9BDZ8	Q9bdz8 bos taurus
15	681	24.6	530	11	Q9R110	Q9r110 cavia porce
16	680.5	24.6	534	11	Q9D811	Q9d811 mus musculu
17	680	24.6	529	6	Q9GLD9	Q9gld9 macaca mula
18	677.5	24.5	534	11	Q8R129	Q8r129 mus musculu
19	674.5	24.4	530	11	Q7TT85	Q7tt85 rattus norv
20	673.5	24.3	533	6	O46548	O46548 felis silve
21	672.5	24.3	449	4	Q9H6S4	Q9h6s4 homo sapien
22	670.5	24.2	528	11	Q80X89	Q80x89 mus musculu
23	670	24.2	527	11	Q9ESE4	Q9ese4 mus musculu
24	668	24.1	529	11	Q8R084	Q8r084 mus musculu
25	667.5	24.1	529	11	Q8VIF8	Q8vif8 cavia porce
26	667	24.1	533	6	O46549	O46549 felis silve
27	666.5	24.1	528	6	Q8WN97	Q8wn97 macaca fasc
28	665.5	24.0	533	6	O46423	O46423 felis silve
29	665	24.0	533	6	Q9TSL7	Q9tsl7 macaca fasc
30	664	24.0	531	11	Q8VD45	Q8vd45 rattus norv
31	662	23.9	533	6	Q95KM4	Q95km4 macaca mula
32	661	23.9	528	11	Q8VIF9	Q8vif9 cavia porce
33	660.5	23.9	529	6	Q9GLE0	Q9gle0 macaca mula
34	658	23.8	533	6	Q9BDG7	Q9bdg7 macaca mula
35	650.5	23.5	532	11	Q8K154	Q8k154 mus musculu
36	643	23.2	529	11	Q8BJL9	Q8bjl9 mus musculu
37	637.5	23.0	530	11	Q91WH2	Q91wh2 mus musculu
38	637.5	23.0	532	4	Q8WUQ4	Q8wuq4 homo sapien
39	635.5	23.0	529	6	O18736	O18736 bos taurus
40	635.5	23.0	530	11	Q8K169	Q8k169 mus musculu
41	634	22.9	530	11	Q8VCN3	Q8vcn3 mus musculu
42	627	22.7	530	6	Q9TSM0	Q9tsm0 macaca fasc
43	624.5	22.6	532	6	Q9TSL9	Q9tsl9 macaca fasc
44	621.5	22.5	498	11	Q8VCQ9	Q8vcq9 mus musculu
45	621	22.4	530	6	Q9TSL8	Q9tsl8 macaca fasc

ALIGNMENTS

RESULT 1

Q8NBP2

ID Q8NBP2 PRELIMINARY; PRT; 523 AA.

AC Q8NBP2;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein NT2RP2002934.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK075383; BAC11583.1; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_gluco_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Hypothetical protein.
SQ SEQUENCE 523 AA; 59618 MW; 89928A26AB9C09F5 CRC64;

Query Match 99.5%; Score 2754; DB 4; Length 523;
Best Local Similarity 99.6%; Pred. No. 8.1e-222;
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Db	1	MAGQRVLLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
Qy	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKGFENLLNVLEYLALQ	120
Db	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKGFENLLNVLEYLALQ	120
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Db	121	CSHFLNRKDIMDSLKNENFDMVIVETFDCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIP	180
Qy	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	181	LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQDLENFIAKFGDSGFVLVTL	300
Db	241	LLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKVPVQDLENFIAKFEDSGFVLVTL	300
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	301	GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShWPKDVHLAANVKIVDWLPQSDLLAH	360
Qy	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Db	361	PSIRLFVTHGGQNSIMEAIQHGVPVVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETL	420
Qy	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480
Db	421	ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPW	480

QY 481 HEQYLFDFVFVFLGLTLGLTLWLWLCGKLLGMAVWWLRGARKVKET 523
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Db 481 HEQYLLDVVFVFLGLTLGLTLWLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 2

Q96DM6

ID Q96DM6 PRELIMINARY; PRT; 523 AA.
AC Q96DM6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ32504.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK057066; BAB71358.1; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_gluco_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Hypothetical protein.
SQ SEQUENCE 523 AA; 59148 MW; 2034D6E90863EA8E CRC64;

Query Match 79.2%; Score 2193; DB 4; Length 523;
Best Local Similarity 78.8%; Pred. No. 7.5e-175;
Matches 413; Conservative 45; Mismatches 64; Indels 2; Gaps 2;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
| ||||| ||| |||||||||||||||:|||||:|||||:||||| |:
Db 1 MVGQRVLLLVAFLLSGVLLSEAAKILTISTLGGSHYLLLD RVSQILQE HGHNV TML-HQS 59

Qy 61 GPFM-PDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLAL 119
| |: || |:||||||| |:||||: || || |:| || |:| |: |||
Db 60 GKFLIPDIKEEEKSYQVIRWFSPEDHQKRIKKHFD SYIETALDGRKESEALVKLMEIFGT 119

Qy 120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKL GKPFVAILSTSEFGSL EFG LPI 179
|||: |:||||||| |:| || |||:| ||||| ||||| |:||||:||||
Db 120 QCSYLLSRKDIMDSLKNENCDLVFVEAFDFCSFLIAEKL VKPFVAILPTTFGSLDFGLPS 179

Qy 180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSF CRRQQHMQSTFDNTIKEHFT EGSRPVLSH 239
||||||| ||||||||||||||||||| | | ||||||||||| |||||||
Db 180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSF SRSQWDMQSTFDNTIKEHFP EGSRPVLSH 239

Qy 240 LLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVT 299
 |||||:|||||:|||||:|||||
 Db 240 LLLKAELWVNSDFAFDFARPLLNTVYIGGLMEKPIKVPQDLNFIANFGDAGFVLVA 299

Qy 300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLA 359
 |||:| |: |: |:|:||||| || |||:||||| |||||
 Db 300 FGSMLNTHQSQEVLKKMHNAFAHLPQGVIWTCQSSHWPDRVHLATNVKIVDWLPQSDLLA 359

Qy 360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAET 419
 |||||:| |:|:|||||:| || ||| ||:||||:| ::|:
 Db 360 HPSIRLFVTHGGQNSVSMETIRHGVPMVGLPVGNDQHGNMVRVAKNYGVSIRLNQVTADT 419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQP 479
 | | |||:||||| ||||| | ||| |||||:|||||
 Db 420 LTLTMKQVIEDKRYKSAVAASVILHSQPLSPAQRLVGWIDHILQTTGGATHLKPYVFQQP 479

Qy 480 WHEQYLFDFVFLGLTLGLTLWLCGKLLGMVWWLRGARKVKET 523
 ||||| |||||:|||||: |||||:
 Db 480 WHEQYLIDVFLGLTLGLTMWLCGKLLGVVARWLRGARKVKKT 523

RESULT 3

Q8ROY5

ID Q8ROY5 PRELIMINARY; PRT; 523 AA.
 AC Q8ROY5;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC025940; AAH25940.1; -.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 523 AA; 59742 MW; F2EF34F41C3DEB95 CRC64;

Query Match 65.6%; Score 1815; DB 11; Length 523;
 Best Local Similarity 65.4%; Pred. No. 3.3e-143;
 Matches 342; Conservative 73; Mismatches 106; Indels 2; Gaps 2;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
 || | ||| | | ||| |||||: |||:|:||||| ||:| | ::
 Db 1 MAAHRSWLLVSFFLLEVLLLEAAKILTISTLSASHYILMNRVSQILQGGGHDVIKLLYEG 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
 | :|||:| ||||:| ||| |: |: : :|| || |: || : :| |

Db 61 GD-IPDFRKENSSYQVINWRLPEDQKTFENRWHRLIDEYAYGRSKYHTLLKIHQYFADL 119

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGLSLEFGLP-I 179
 ||| |:||||: |: ||||:|::: | | ||| |||| ||: | | ::|||

Db 120 CSHLLSRKDIMELLQKENFDLVLLDSMDLCSFLIVEKLGKRFVSFLPFQFSYMDFGLPNA 179

Qy 180 PLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSH 239
 |||| ||: | ||| ||||| |||| | ::: : | : ||:| |||:||||

Db 180 PLSYAPVYGSLTDQMDFWGRVKNILMFFHFTKKRRDIFSQYGNTVQEHFAEGSQPVLS 239

Qy 240 LLLKAELWFINSDFAFDFARPLLPNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVT 299
 ||||| |||: |||| | ||||| |||||: ||: ||: |||||: ||: ||||| |||||

Db 240 LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLEDFISQFGDSGFVLVA 299

Qy 300 LGSMVNTCQNPEIFKEMNNAFAHLPGQVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLA 359
 | |:|: |: || ||||:||||||| ||: | ||||| || ||||:|||| ||||

Db 300 LDSVSMIQSKEI IKEMNSAFAHLPGQVLWTCSSHWPKDVSLAPNVKIMDWLPQIDLLA 359

Qy 360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAET 419
 ||||| ||||| ||: ||: ||||| ||||| ||||| ||||| |||||: ||||:

Db 360 HPSIRLFVTHGGMNSVMEAVHHGVPMVGIPFFGDQPENMVRVEAKNLGVSIQLQTLKAES 419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQP 479
 | ||::||: ||: ||: || || ||||: | ||||| ||||| ||||| ||||

Db 420 FLLTMKEVIEDQRYKTAAMASKVIRNSHPLTPAQRVLGWIDHILQTGGAHLKPYAFQQP 479

Qy 480 WHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
 ||||: ||: ||||| ||||| |: | : | |||:

Db 480 WHEQYMLDVFLGLTLGLTLWLSVKVLVAVTRYLSISRKVQ 522

RESULT 4

Q8JZZ0

ID Q8JZZ0 PRELIMINARY; PRT; 523 AA.

AC Q8JZZ0;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein MGC37820.

GN AI313915.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC034837; AAH34837.1; -.

DR MGD; MGI:2145969; AI313915.

DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002213; UDP_gluco_trans.

DR Pfam; PF00201; UDPGT; 1.

DR PROSITE; PS00375; UDPGT; 1.

KW Hypothetical protein.

SQ SEQUENCE 523 AA; 59662 MW; 4F7BD5ACBAFB5127 CRC64;

Query Match 65.2%; Score 1804; DB 11; Length 523;
Best Local Similarity 65.4%; Pred. No. 2.7e-142;
Matches 342; Conservative 69; Mismatches 110; Indels 2; Gaps 2;

```
Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
      || | ||: || |:| ||||| ||||: |||::: ||||:| : |||| | ::
Db      1 MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      :||:|:|: ||||:| ||| :::| || || | || : :|
Db     61 AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL 119

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLP-I 179
      || |:||||| |||||:|:|:| || ||||| ||: | | :|||
Db    120 CSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGKRFVSFLPFQFSYMDFGLPISA 179

Qy    180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQOHMQSTFDNTIKEHFTEGSRPVLSH 239
      |||| ||: | ||| ||||| ||||| | :|: : | :|:|:| ||| :|||
Db    180 PLSYAPVYGSLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSQPVLS 239

Qy    240 LLLKAELWFINSDFAFDFARPLLPNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVT 299
      ||||| ||||: ||||| ||||| ||||| ||||: ||||: ||||: ||||: ||||: ||||
Db    240 LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLENFISQFGDSGFVLVA 299

Qy    300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCSEHWPKDVHLAANVKIVDWLPQSDLLA 359
      |||:|: |: || ||||: ||||| ||||: | |: ||||| ||: ||||: ||||: ||||
Db    300 LGSIVSMIQSKEIIKEMNSAFAHLPQGVLTCTSHWPKDVSLASNVKIMDWLPQTDLLA 359

Qy    360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAET 419
      ||||| ||||| ||: |||: ||||| ||||| ||||| ||||| ||||| ||||: ||||:
Db    360 HPSIRLFVTHGGMNSVMEAVHHGVPMVGIPFFFDQPENMVRVEAKNLGVSIQLQTLKAES 419

Qy    420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKPYPVFQQP 479
      || ||:|: ||||| ||||: |: | ||||: | ||: ||||: ||||| ||||| ||||
Db    420 FALTMKKIIEDKRYKSAAMASKIIRHSHPLTPAQRLVGWIDHILQTTGAAHLKPYAFQQP 479

Qy    480 WHEQYLFDFVFLVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
      ||||: |||: |||| ||||| |:| :| | ||||
Db    480 WHEQYMLDVFLVFLGLMLGLTLWLWSVKVLVAVTRYLSIATKVKE 522
```

RESULT 5

Q8VC11

ID Q8VC11 PRELIMINARY; PRT; 523 AA.

AC Q8VC11;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein (Hypothetical UDP-glucoronosyl and UDP-glucosyl
transferase containing protein).

GN AI313915.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; BC022134; AAH22134.1; -.
 DR EMBL; AK050128; BAC34080.1; -.
 DR MGD; MGI:2145969; AI313915.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 523 AA; 59672 MW; BC7BD6ADF197ADD9 CRC64;

Query Match 65.1%; Score 1802; DB 11; Length 523;
 Best Local Similarity 65.4%; Pred. No. 4e-142;
 Matches 342; Conservative 68; Mismatches 111; Indels 2; Gaps 2;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR	60
		: : : : : :	
Db	1	MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES	60
Qy	61	GPFMPDFKKEEKSQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120
		: : : : : : : :	
Db	61	AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL	119
Qy	121	CSHFNLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLP-I	179
		: : : : :	
Db	120	CSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGKRFVSFLPFQFSYMDFGFLPSA	179
Qy	180	PLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSH	239
		: : : : : :	
Db	180	PLSYAPVYGSGLTQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSQLPVLSD	239
Qy	240	LLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKVPQDLENFIAKFGDSGFVLVT	299
		: : : : :	
Db	240	LLLKAELWVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLENFISQFGDSGFVLVA	299
Qy	300	LGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLA	359
		: : : : : : : :	
Db	300	LGSIVSMIQSKEIIKEMNSAFAHLPQGVLTCTSHWPKDVSLAPNVKIMDWLPQTDLLA	359
Qy	360	HPSIRLFVTHGGQNSIMEAIQHGVPVMGIPFLGDPENMVRVEAKKFGVSIQLKKLKAET	419
		: : : :	
Db	360	HPSIRLFVTHGGMNSVMEAVHHGVPVMGIPFFFDQPENMVRVEAKNLGVSIQLQTLKAES	419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQP 479
 || ||:|:|||||||:|: | |||:| |||:||||:||||| |||| ||||
 Db 420 FALTMKKIIEDKRYKSAAMASKIIRHSHPLTPAQRLLGWIDHILQTGGAAHLKPYAFQQP 479
 Qy 480 WHEQYLFDFVFLGLTLGLTLWLCLCGKLLGMAVWWLRGARKVKE 522
 |||||: |||:|||| | |||| | |: | :| | ||||
 Db 480 WHEQYMLDVFLFLLGLMLGLTLWLSVKVLVAVTRYLSIATKVKE 522

RESULT 6

Q8NAW4

ID Q8NAW4 PRELIMINARY; PRT; 221 AA.
 AC Q8NAW4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ34658.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isogai T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK091977; BAC03783.1; -.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 221 AA; 24764 MW; ACB59BEF47ACD458 CRC64;

Query Match 34.8%; Score 963; DB 4; Length 221;
 Best Local Similarity 79.6%; Pred. No. 2.1e-72;
 Matches 176; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 303 MVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLLAANVKIVDWLPQSDLLAHPS 362
 |:| | : | : |:|:||||||| || |||:|||| | ||||| ||||| |||||
 Db 1 MLNTHQSQEVLKKMHNAFAHLPQGVIWTCQSSHWPRDVHLATNVKIVDWLPQSDLLAHPS 60
 Qy 363 IRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAETIAL 422
 ||||| |||||:||||:|||||:|: ||| |||| | | :|||:| :| :||| |
 Db 61 IRLFVTHGGQNSVMEAIRHGVPMVGLPVNGDQHGNMVRVVAKNYGVSIIRLNQVTADTLTL 120
 Qy 423 KMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHE 482
 |||:|:||||| ||||| | |||| | |||||:||||||| |||||


```

Db      121  TMKQVIEDKRYKSAVVAASVILHSQPLSPAQRLVGWIDHILQTGGATHLPYAFQQPWHE 180
Qy      483  QYLFDFVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKET 523
        ||| ||||| ||||| : ||||| : ||||| : |
Db      181  QYLIDVFVFLLGLTLGTMWLCLGKLLGVVARWLRGARKVKKT 221

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RESULT 7

```

Q8IYS9
ID   Q8IYS9          PRELIMINARY;          PRT;   252 AA.
AC   Q8IYS9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC035012; AAH35012.1; -.
DR   GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002213; UDP_gluco_trans.
DR   Pfam; PF00201; UDPGT; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 252 AA; 29155 MW; 956CC9F9718B8982 CRC64;

```

Query Match 33.0%; Score 914.5; DB 4; Length 252;
Best Local Similarity 75.7%; Pred. No. 2.9e-68;
Matches 171; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

Qy	58	HKRGPFM-PDFKKEEKSQVISWLAPEDHQREFKKSDFDFLEETLGGRGKFENLLNVLEY	116
		: : : : : : : ::	
Db	3	HQSGKFLIPDIKEEEKSYQVIRWFSPEDHQKRIKKHFDSYIETALDGRKESEALVKLMEI	62
Qy	117	LALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFG	176
		: : : :	
Db	63	FGTQCSYLLSRKDIMDSLKNENYDLVFVEAFDFCSFLIAEKLVKKPFVAILPTTFGSLDFG	122
Qy	177	LPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPV	236
Db	123	LPSPLSYVPVFPSSLTDHMDFWGRVKNFLMFFSFQRSQWDMQSTFDNTIKEHFPEGSRPV	182
Qy	237	LSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLEMEKPIKVPVQD	282
Db	183	LSHLLLKAELWFVNSDFAFDFARPLLNTVYIGGLEMEKPIKVPVQN	228

RESULT 8

Q8BRY7
ID Q8BRY7 PRELIMINARY; PRT; 302 AA.
AC Q8BRY7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing
 DE protein.
 GN AI313915.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK041045; BAC30796.1; -.
 DR MGD; MGI:2145969; AI313915.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 302 AA; 35256 MW; C78A84C1D58987DC CRC64;

Query Match 28.6%; Score 792; DB 11; Length 302;
 Best Local Similarity 57.9%; Pred. No. 6.7e-58;
 Matches 157; Conservative 37; Mismatches 75; Indels 2; Gaps 2;

Qy 1 MAGQRVLLLVGFLLPVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKKR 60
 || | ||: || |:| ||||| |||: |||:| : |||| | :
 Db 1 MAAHRRWLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES 60

 Qy 61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
 :|||:|: ||||:| ||| :|: || || | || : :|
 Db 61 AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL 119

 Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGLSLEFGLP-I 179
 || |:||||| |||||:|:|:| | | || |||| ||: | | :|||
 Db 120 CSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGKRFVSFLPFQFSYMDFGLPSPA 179

 Qy 180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFERRQQHMQSTFDNTIKEHFTEGSRPVLSH 239
 |||| ||: | ||| ||||| ||||| | :|: : | :|:|:| ||| :|||
 Db 180 PLSYAPVYGSGGLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSPVLSD 239

 Qy 240 LLLKAELWFINSDFAFDFARPLLNTVYVVG 270
 ||||| |||: |||| | |||| | |||||
 Db 240 LLLKAELWFVNSDFALDFARPLFPNTVYVVG 270

RESULT 9

Q98TB5

ID Q98TB5 PRELIMINARY; PRT; 541 AA.
 AC Q98TB5;

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DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      UDP-galactose ceramide galactosyltransferase (EC 2.4.1.47).
GN      CGT.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kapitonov D.;
RT      "Molecular cloning and expression of ceramide galactosyltransferases.
RT      Comparison with other glycosyltransferases.";
RL      Thesis (1997), Medical College of Virginia, Richmond, VA, USA.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Kapitonov D.;
RL      Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF129809; AAK16234.1; -.
DR      GO; GO:0047263; F:N-acylsphingosine galactosyltransferase act. . .; IEA.
DR      GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR      GO; GO:0008152; P:metabolism; IEA.
DR      InterPro; IPR002213; UDP_gluco_trans.
DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Glycosyltransferase; Transferase.
SQ      SEQUENCE      541 AA;  61598 MW;  DFF1CA4C69E781CC CRC64;

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Qy	13	LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHNVMTLNHKGPFMPDFKKEE	71
Db	11	LWSAVGIARAANKIVVPPIMFESHLYIFKTLASALHDQGHQTVFLLSEGREIPPSNHYRL	70
Qy	72	KSYQVISWLAPEDHQREFKKS-FDFFLEETL----GGRGKFENLLNVLEYLALQCSHFLN	126
Db	71	KRYPGI-----FNSSTSDDFLQSKMRSIFSGRLTALELFDILDHYSKNCDMIVG	119
Qy	127	RKDIMDSLKNEFDMVIVETFDYCPFLIAEKLKGPFAVAILSTSFGSLEFGLPIPLSYVPV	186
Db	120	NQNLMHALKQEKFDLLLVDPNEMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPAPLSYVPE	179
Qy	187	FRSLLTDHMDFWGRVKNFLMF-----FSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	180	FNSLLTDRMNLFERMKNFTFVYVISRFGVSFL-----VLPKYERIMQKHKVLPERSMYD-L	233
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL	300
Db	234	VHGSSLWMLCTDIALEFFRPRTLPNVVYVGILTKPASPLPEDLQTWVNGANENGFVLVSF	293
Qy	301	GSMVNTCQNPEIFKEMNNAFAHLPGQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH	360
Db	294	GAGVKYL-SEDVANKLARALARLPORVIWRFSGN---KPRNLGNNTKLIIEWLPONDLLGH	349


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Db      113 NCDMMVGNQALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172
Qy      180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH-----MQSTFD 222
      ||: ||| | |||| |:| |:| ||: | | | :| :|
Db      173 PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRIGVSFLVLPKYERIMQKYNLLPAKSMYD 232
Qy      223 NTIKEHFTEGSRPVLSHLLLLKAELWFINSDFAFDFARPLLNPNTVYVGGLMKPKPKVPQD 282
      |: | : || : :| | :| || ||| ||||: : || |:| :|
Db      233 -----LVHGSSLWMLCTDVALEFPRPTLPNVVYVGGILTKPASPLPED 275
Qy      283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIIWKQCQSHWPKDVHL 342
      |: :: : ||||: |:| : :| :: | || ||| : | :|
Db      276 LQRWVSGAQEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---KPKNL 331
Qy      343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVE 402
      | |::: ||||: ||| | :|| |: ||| || | : ||||: ||||| | : | ||:
Db      332 GNNTKLIEWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVPPVVGIPPLFGDHYDTMTRVQ 391
Qy      403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      || |: : : : | : : : : |: | | | : | | | |||:
Db      392 AKGMGILLEWNTVTEGELYDALVKVINNPSYRQRAQKLSEIHKDQPGHPVNRTTYWIDYI 451
Qy      463 LQTGGATHLKPYPVFQQPWHEQYLFQDV-FVFLGLGLTL 497
      |: || ||: | | : : :| |: || ||| |
Db      452 LRHDGARHLRSVHVQISFCQYFLLDIAFVLLLGAVL 487

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RESULT 11

Q9TSL6

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ID   Q9TSL6          PRELIMINARY;          PRT;    529 AA.
AC   Q9TSL6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   UDP-glucuronosyltransferase 2B23 (EC 2.4.1.17).
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20043918; PubMed=10579317;
RA   Barbier O., Levesque E., Belanger A., Hum D.W.;
RT   "UGT2B23, a novel uridine diphosphate-glucuronosyltransferase enzyme
RT   expressed in steroid target tissues that conjugates androgen and
RT   estrogen metabolites.";
RL   Endocrinology 140:5538-5548(1999).
DR   EMBL; AF112113; AAF14353.1; -.
DR   GO; GO:0015020; F:glucuronosyltransferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002213; UDP_gluco_trans.
DR   Pfam; PF00201; UDPGT; 1.
DR   PROSITE; PS00375; UDPGT; 1.
KW   Glycosyltransferase; Transferase.
SQ   SEQUENCE    529 AA;  60957 MW;  646315E6D970541A CRC64;

```

Query Match 24.9%; Score 689.5; DB 6; Length 529;
 Best Local Similarity 32.1%; Pred. No. 5.5e-49;
 Matches 168; Conservative 85; Mismatches 205; Indels 65; Gaps 14;

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Qy      34 SHYLLMDRVSQILQDHGHNVTML-----NH----KRGPFMPDFKKEE----KSYQ 75
      ||:: | : : | || || | : | | : :
Db      34 SHWMNMKTILEELVQRGHEVTALASSASILFDPNNSSALKIEVFPTSLPKPEFENIVTQE 93

Qy      76 VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSL 134
      : | : | : | : | : | : | : | : | : | : | : |
Db      94 IKRWIELPKD-----TFWLYFSQMQEIMWKFGDIFRNF-----CKDVVSNKKLMKKL 140

Qy     135 KNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEF-----GLPIPLSY 183
      : ||:| : | :|| | | | : || | | | | | | | |
Db     141 QESRFDVVFADPIFPCSELLAELFNIPLVY-----SLRFTPGYVFEKHCGGFLFPPSY 193

Qy     184 VPFVRSLLTDHMDFWGRVKN--FLMFFSFCRRQOHMQSTFDNTIKEHFTE--GSRPVLSH 239
      ||| | | :| | | |||| :::| || : | : : :|| | ||
Db     194 VPVVMSELSDQMTFMERVKNMIMLYDFDFCFQIYDMKKW-----DQFYTEVLGRHTTLSE 248

Qy     240 LLLKAELWFINSDFAFDFARPLLNTVYVGGLEMEKPIKVPQDLENFIAKFGDSGFVLVT 299
      :: ||::| | : : | | |||| :::| | | | :::| | : | : |
Db     249 IMGKADIWLIRNSWNFQFPHPLLPNVDFIGLLCKPAKPLPKEMEETFVQSSGENGVVFT 308

Qy     300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLA 359
      ||||: | | : : | :|| | : : | | | : | : | : | : |
Db     309 LGSMI-TNMKEERANVIASALAQIPQKVLWRFDGN---KPDTLGVNTRLYKWIPQNDLLG 364

Qy     360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAET 419
      || : : |||| | | ||| ||||| ||||| ||||: : : : | : : :
Db     365 HPKTKAFITHGGANGIYEAIYHGVPMVGIPLFADQPDNIAHMKTRGAAVQLDFDTMSSTD 424

Qy     420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQP 479
      | : | : : | | : | | | | : | | | : | : | | | : |
Db     425 LVNALKTVINDPLYKENVMKLSRIQRDQPVKPLDRAVFWIEFVMRHKGAKHLRPAAHDLT 484

Qy     480 WHEQYLFDFVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKE 522
      | : : ||| ||| ::: | | : ||| | :
Db     485 WFQYHSFDVIGFLLACVATVIFIIMKCLFCFW--KFARKGKK 525

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RESULT 12

O97951

ID O97951 PRELIMINARY; PRT; 529 AA.

AC O97951;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE UDP-glucuronosyltransferase.

GN UGT2B18.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RA Beaulieu M., Levesque E., Barbier O., Turgeon D., Belanger G.,
 RA Hum D.W., Belanger A.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF016310; AAC98726.1; -.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase.
 SQ SEQUENCE 529 AA; 60801 MW; 3ECEB497B8C3601F CRC64;

Query Match 24.8%; Score 685.5; DB 6; Length 529;
 Best Local Similarity 33.2%; Pred. No. 1.2e-48;
 Matches 173; Conservative 75; Mismatches 212; Indels 61; Gaps 14;

Qy	34	SHYLLMDRVSQILQDHGHNVTML-----NH----KRGPFMPDFKKEEKS----YQ	75
		: : : : :	
Db	34	SHWMNMKTILEELVQRGHEVTVLASSASILFDPNNSALKIEVFPTSLTKTEFENIIRQQ	93
Qy	76	VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSL	134
		: : : : : : : :	
Db	94	IKRWSELPKD-----TFWLYFSQMQEIMWKFGDITRNF-----CKDVVSNNKKLMKKL	140
Qy	135	KNENFDMVIVETFDYCPFLIAEKLKGFVAILSTSFGSLEF-----GLPIPLSY	183
		: : :	
Db	141	QKSREDFVVFADAI FPCSELLAELLNTPLVY-----SLRFTPGYNFEKHCGGFLFPFSY	193
Qy	184	VPVFRSLLTDHMDFEWGRVKN--FLMFFSFCCRQOHMQSTFDNTIKEHFTEGSRPVLSHLL	241
		: : :	
Db	194	VPVVMSELSDHMTFMERVKNMIYMLYDFDC-FQIYAMKKWDQFYSE--VLGRPTTLSETM	250
Qy	242	LKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLG	301
		: : : : : : : : :	
Db	251	GKADIWLIRNSWNFQFPHPLLPNVDFVGGHLHCKPAKPLPKEMEETFVQSSGENGVVVFSLG	310
Qy	302	SMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShwPKDVHLAANVKIVDWLPQSDLLAHP	361
		: : : : : : :	
Db	311	SMV-TNMKEERANVIASALAIQIPQKVLWRFD---GKKPDTLGLNTRLYKWIPQNDLLGHP	366
Qy	362	SIRLFVTHGGQNSIMEAIQHGVPVMGVIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLA	421
		: : : : :	
Db	367	KTRAFITHGGSGNGIYEAIYHGVPVMGVIPLFADQPDNIAHMKAKGAAVRLDFDTMSSTDLV	426
Qy	422	LKMKQIMEDKRYKSAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWH	481
		: : : : : : :	
Db	427	NALKTVINDPLYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRPAHADLTWF	486
Qy	482	EQYLFDFVVFLLGLTLGLTLWLCCGKLLGMAVWWLRGARKVKE	522
		: : : : :	
Db	487	QYHSLDVIGFLLACVATVIFIIMKCCLFCFW--KFARKGKK	525

RESULT 13

Q8BWQ1

ID Q8BWQ1 PRELIMINARY; PRT; 534 AA.

AC Q8BWQ1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to UDP glucuronosyltransferase UGT2A3.
 GN 2010321J07RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK050327; BAC34191.1; -.
 DR MGD; MGI:1919344; 2010321J07Rik.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 SQ SEQUENCE 534 AA; 61119 MW; 3BF4F591395B1620 CRC64;

Query Match 24.8%; Score 685.5; DB 11; Length 534;
 Best Local Similarity 33.5%; Pred. No. 1.2e-48;
 Matches 171; Conservative 83; Mismatches 195; Indels 61; Gaps 13;

Qy	34	SHYLLMDRVSQILQDHGHNVTMLNH-----KRGPFMPDFKKEEKSYQVIS	78
		: : : : : : : : : : :	
Db	34	SHWLNKLTILEELGARGHEVTVLKYPSSIIDQSKRIPLHFENIPLLYEIETAENRLNEIA	93
Qy	79	WLA----PEDHQREFKKSF-DFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMS	133
		: : : : : :	
Db	94	NLAVNVIPNLSLWEAAKTLDQDFLQVT----GDFESI-----CRSVLYNQKFMDK	139
Qy	134	LKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFG---SLEFG-LPIPLSYVPVFRS	189
		: : : : : : :	
Db	140	LRDAQYDVVVIDPVVPCGELVAEVLQIPFVYTLRFSGMGYYMEKHCGQLPIPLSYVPVMS	199
Qy	190	LLTDHMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHF---TEGSRPVLSHLLLKA	244
		: : : : : : :	
Db	200	ELTDNMTFTERVKNMMFSLLEFYWLQQ-----YDFAFDQFYSETLGRPTTFCKTVGKA	253
Qy	245	ELWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV	304
		: : : : : : : : : : : :	
Db	254	DIWLIRTYWDVEFRPYLPNFEEFVGGHLCKPAKPLPKEMEETFVQSSGEHGVVVSIGSMV	313
Qy	305	NTCQNPEIFKEMNNAFAHLPQGVIWKQCShwPKDVHLAANKIVDWLPQSDLLAHPSIR	364
		: : : : : : : : : : : :	
Db	314	KNL-TEEKANLIASVLAQIPQKVLWRYS---GKKPATLGSNTRLFNWIPQNDLLGHPKTK	369
Qy	365	LFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKM	424


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      |:||| | | || | |||||:|: ||| |: :||| : : : : : | :
Db      370 AFITHGGTNGIYEAIYHGVPMVGVPMGLDQPHNIAHMEAKGAALKVSISTMTSTDLLSAV 429

Qy      425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQY 484
      : : : | | |: | | |: | | | |: |: | | |: | : :
Db      430 RAVINEPSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAHDLSWFQYH 489

Qy      485 LFDVVFVFL-----GLTLGTLWLCGKL 506
      || ||| :| |:| ||
Db      490 SLDVIGFLLLCVVTLTFTIITKFCLEVCQKL 519

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RESULT 14

Q9BDZ8

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ID      Q9BDZ8      PRELIMINARY;      PRT;      498 AA.
AC      Q9BDZ8;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      UDP-galactose ceramide galactosyltransferase (EC 2.4.1.47)
DE      (Fragment).
GN      CGT.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kapitonov D.;
RT      "Molecular cloning and expression of ceramide galactosyltransferases.
RT      Comparison with other glycosyltransferases.";
RL      Thesis (1997), Medical College of Virginia, Richmond, VA, USA.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Kapitonov D.;
RL      Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AF129810; AAK16235.1; -.
DR      GO; GO:0047263; F:N-acylsphingosine galactosyltransferase act. . . ; IEA.
DR      GO; GO:0016758; F:transferase activity, transferring hexosyl . . . ; IEA.
DR      GO; GO:0008152; P:metabolism; IEA.
DR      InterPro; IPR002213; UDP_gluco_trans.
DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Glycosyltransferase; Transferase.
FT      NON_TER      1      1
SQ      SEQUENCE      498 AA; 56674 MW; 83645A7079ACF582 CRC64;

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Query Match      24.7%; Score 684.5; DB 6; Length 498;
Best Local Similarity 32.8%; Pred. No. 1.3e-48;
Matches 161; Conservative 92; Mismatches 173; Indels 65; Gaps 12;

Qy      58 HKRGPFMPDFKKEEKSYQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGK 106
      |:|| : | : :||:| : : | | |: : ||
Db      3 HERGHHTVFLRSEGRD-----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLT 56

Qy      107 FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVFVAIL 166

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      ||::||: | : : || |||:::| | ||| | | :
Db      57 AIELLDILDHYTKSCDMVGNHALIQGLKQENFDLLLVDPNMCGFLIAHLLGVKYAVFS 116
Qy      167 STSFGSLEFGLPIPLSYVPVFRSLTDMDFWGRVKN-----FLMFFSFCRRQ 214
      : : | | | ||:| | | |||||: |:|| | | : |
Db      117 TGLWYPAEVGAPAPLAYVPEFNSLLTDHMNLLQRMKNTGVYLISRIGISFLVLPKYERIM 176
Qy      215 QHM-----QSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVG 269
      | : : | : : || : : | | : | | | | | |
Db      177 QEYNLLPEKSMYD-----LVYGSSLWMLCTDVALEFPRTLPNVVYVG 219
Qy      270 GLMEKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIV 329
      |:| || |:|:| : : : ||||: | : | : : | | | | |
Db      220 GILTKPASPLPEDFQRWVNGANEHGFVLVSFGAGVKYL-SEDIATKLAGALGRLPQKVIW 278
Qy      330 KCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQNSIMEAIQHGVPVVGIP 389
      : : | : | : : ||||| | : | : : || | | : | | : | | |
Db      279 RFSGT---KPKNLGNNTRLIEWLPQNDLLGHSNIKAFLSHGGLNSIFETMYHGVPVVGIP 335
Qy      390 LFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPL 449
      ||| : |:|:| | : : | : | : : : | : | | :
Db      336 LFGDHYDTMIRVQAKGMGILLEWKTVTEGELYEALVKVINNPYSYRQRAQKLSEIHKDQLR 395
Qy      450 SPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLED-VFVFLLG-----LTLGTLW 501
      | | | ||::|: || |:| | : : : | | || | | | : | :
Db      396 HPVNRTVYWIDYILRHDAHHIRAAVHQISFCQYFLLDIVFVLLLGAALFYLLSWVTKF 455
Qy      502 LCGKLLGMAVW 512
      :| :: :|
Db      456 ICRRI--RSLW 464

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RESULT 15

Q9R110

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ID   Q9R110          PRELIMINARY;          PRT;    530 AA.
AC   Q9R110;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   UDP glucuronosyltransferase UGT2A3.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Hartley; TISSUE=Liver;
RX   MEDLINE=99410697; PubMed=10479484;
RA   Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;
RT   "Morphine regulation of a novel uridine diphosphate glucuronosyl-
RT   transferase in guinea pig pups following in utero exposure.";
RL   Mol. Genet. Metab. 68:68-77(1999).
DR   EMBL; AF175221; AAD51732.1; -.
DR   GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002213; UDP_gluco_trans.

```

DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase.
SQ SEQUENCE 530 AA; 59895 MW; EE2F394D3FD484E1 CRC64;

Query Match 24.6%; Score 681; DB 11; Length 530;
Best Local Similarity 32.2%; Pred. No. 2.9e-48;
Matches 168; Conservative 88; Mismatches 227; Indels 38; Gaps 11;

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Qy      13 LLPGVLLSEAAKILTISTVGG-----SHYLLMDRVSQILQDHGHNVTMLNHKR 60
      : || | | : | | | | | | | | | | | | | | | | | | | | | |
Db      1 MAPGKLASAVLLLLCCAGSGFCGKVLVWPCEMSHWLNKLTLEELVKRGHEVTVLTLSN 60

Qy     61 GPFMPDFKKEEKSQVISWLAPEHQREFKKSFDFFLEETL-----GGRGKFENL 110
      | : : : : | | : : | : | : : : | : :
Db     61 NLFIDYNRHPAFNFVIP--VPTDKNMS-ENILNEFIELAVNVMPMTPLWQSGKLLQQFF 117

Qy    111 LNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSF 170
      : : | | | | : : : : | | : : | : : : : | | : | | | | : | |
Db    118 VQITEDLGLNCRNTVYNQSLMKKLKRDSDYDVLVTDVPVPCGELVAEMLGVFPVNMLKFSM 177

Qy    171 G-SLE---FGLPIPLSYVPVFRSLTDMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNT 224
      | : : | | | | | | | | | | | | | | | | : | | | : |
Db    178 GHTIEKYCGQLPAPPSYVPVPLGGLTTRMTFMERVKNMVFSVLFDFW-IQQYDYKFWQDF 236

Qy    225 IKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLE 284
      | | | | : : | | : : | : | | | | : | | | | | | | | : : |
Db    237 YSEAL--GRPTTLCEIMGKAEIWLIRTYWDFEFPRPYLPNFEFVGGHLCKPAKPLPKEME 294

Qy    285 NFIKFGDGSFVLVTLGSMVNTCQNPFIKEMNNAFAHLPQGVWKCQCQSHWPKDVHLAA 344
      | : | : | : | | | | | : : | : | : | : | : | : | |
Db    295 EFVQSSGEDGVVVFSLGSMVKNL-TEEKANLIASALAQIPQKVLWRYK---GKKPATLGP 350

Qy    345 NVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAK 404
      | : : | : | : | | | : | : | | | | | | | : | | | : : | |
Db    351 NTRLFDWIPQNDLLGHPKTKAFITHGGSNGIYEAIYHGVPMVGMPIFSDQPDNLAGMKAK 410

Qy    405 KFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQ 464
      | : : : : | : : : : | | | : | | | : | | | : : | :
Db    411 GAAVEVNMNTMTSADLLGALRTVINDDPTYKENAMKLSRIHHDQPVKPLDRAAFWVEFVMH 470

Qy    465 TGGATHLKPYVFQQPWHEQYLFDFVFVLLGLTLGLTLWLCGK 505
      | | | : | : : | | | | : | |
Db    471 HKGAKHLRVAHDLSWFQYHSLDVIGFLLACVASAILLVTK 511
```

Search completed: May 7, 2004, 17:32:49
Job time : 48 secs

OM protein - protein search, using sw model

Run on: May 7, 2004, 17:25:14 ; Search time 17 Seconds
(without alignments)
1601.923 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	748.5	27.0	502	1 UDC1_RABIT	P36514 oryctolagus
2	699	25.3	541	1 CGT_HUMAN	Q16880 homo sapien
3	697	25.2	541	1 CGT_MOUSE	Q64676 mus musculu
4	684	24.7	541	1 CGT_RAT	Q09426 rattus norv
5	679	24.5	533	1 UD11_HUMAN	P22309 homo sapien
6	677.5	24.5	530	1 UDB2_RAT	P08541 rattus norv
7	673	24.3	530	1 UDBK_MACFA	O77649 macaca fasc
8	670	24.2	531	1 UDBD_RABIT	P36512 oryctolagus
9	669	24.2	535	1 UD11_MOUSE	Q63886 mus musculu
10	668	24.1	529	1 UDB1_RAT	P09875 rattus norv
11	665	24.0	531	1 UD15_RAT	Q64638 rattus norv
12	664.5	24.0	528	1 UDBJ_MACFA	Q9xt55 macaca fasc
13	663.5	24.0	529	1 UDB9_MACFA	O02663 macaca fasc
14	662.5	23.9	530	1 UDBE_RABIT	P36513 oryctolagus
15	661.5	23.9	528	1 UDB4_HUMAN	P06133 homo sapien
16	658	23.8	533	1 UD12_RAT	P20720 rattus norv
17	658	23.8	535	1 UD11_RAT	Q64550 rattus norv

18	657	23.7	530	1	UDBH_HUMAN	O75795	homo sapien
19	654.5	23.6	529	1	UDB7_HUMAN	P16662	homo sapien
20	651	23.5	527	1	UDA1_HUMAN	Q9y4x1	homo sapien
21	650	23.5	527	1	UDA1_RAT	P36510	rattus norv
22	649	23.4	523	1	UDBG_RABIT	O19103	oryctolagus
23	649	23.4	530	1	UDBF_HUMAN	P54855	homo sapien
24	642	23.2	528	1	UDBA_HUMAN	P36537	homo sapien
25	642	23.2	531	1	UD13_RAT	Q64637	rattus norv
26	639	23.1	530	1	UDB6_RAT	P19488	rattus norv
27	639	23.1	533	1	UD12_MOUSE	P70691	mus musculu
28	638.5	23.1	532	1	UD16_HUMAN	P19224	homo sapien
29	637.5	23.0	530	1	UDB5_MOUSE	P17717	mus musculu
30	636.5	23.0	529	1	UDBS_HUMAN	Q9by64	homo sapien
31	635	22.9	534	1	UD15_HUMAN	P35504	homo sapien
32	634	22.9	530	1	UDB3_RAT	P08542	rattus norv
33	632.5	22.9	530	1	UDBC_RAT	P36511	rattus norv
34	631	22.8	530	1	UD18_HUMAN	Q9haw9	homo sapien
35	629	22.7	520	1	UD17_MOUSE	Q62452	mus musculu
36	624.5	22.6	534	1	UD13_HUMAN	P35503	homo sapien
37	623.5	22.5	529	1	UDBB_HUMAN	O75310	homo sapien
38	623	22.5	531	1	UD17_RAT	Q64633	rattus norv
39	621	22.4	530	1	UD1A_HUMAN	Q9haw8	homo sapien
40	617	22.3	530	1	UD18_RAT	Q64634	rattus norv
41	615.5	22.2	532	1	UD14_RABIT	Q28612	oryctolagus
42	614	22.2	530	1	UD12_HUMAN	P36509	homo sapien
43	612	22.1	530	1	UD17_HUMAN	Q9haw7	homo sapien
44	612	22.1	530	1	UD19_HUMAN	O60656	homo sapien
45	611.5	22.1	531	1	UD16_MOUSE	Q64435	mus musculu

ALIGNMENTS

RESULT 1

UDC1_RABIT

ID UDC1_RABIT STANDARD; PRT; 502 AA.
AC P36514;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UDP-glucuronosyltransferase 2C1 microsomal (EC 2.4.1.17) (UDPGT)
DE (Fragment).
GN UGT2C1 OR UGT2A2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=93315511; PubMed=8325897;
RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
RT "Cloning and characterization of rabbit liver UDP-
RT glucuronosyltransferase cDNAs. Developmental and inducible expression
RT of 4-hydroxybiphenyl UGT2B13.";
RL J. Biol. Chem. 268:15260-15266(1993).
CC -!- FUNCTION: UDPGT is of major importance in the conjugation and

CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; L01083; AAA18023.1; -.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
 KW Multigene family; Microsome.
 FT NON_TER 1 1
 FT TRANSMEM 466 481 POTENTIAL.
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 502 AA; 57449 MW; B6E65670BFAE1D35 CRC64;

Query Match 27.0%; Score 748.5; DB 1; Length 502;
 Best Local Similarity 35.4%; Pred. No. 3.4e-51;
 Matches 180; Conservative 82; Mismatches 178; Indels 69; Gaps 14;

Qy 34 SHYLLMDRVSQILQDHGHNV-----MLNHKRGPFMPDFKK-----EE----- 71
 ||::: : : : || || :| :|:| : || : : ||
 Db 7 SHWINLKVILEELQLRGHEITVLVPSPLLLDHTKIPFNVEVLQLQVTKETLMEELNTVL 66

 Qy 72 --KSYQV--ISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNR 127
 |::: :|| | | | :|| | | :
 Db 67 YMSSFELPTLSWWKVLGKMVEMGKQFS-----KNLRRV-----CDSAITSN 106

 Qy 128 KDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLE----FGLPIPLSY 183
 |:::| || ||: : : :| |::| | || |:: | || | ||
 Db 107 KELLDRLKAAKFDICLADPLAFCELGELVAELLNIPFVYSFRFSIGNIERSCAGLPTPSSY 166

 Qy 184 VPFVRSLLTDHMDFWGRVKNFLMFFSFCRRQQH-MQSTFDNTIKEHFTE--GSRPVLSHL 240
 || | ||:| | |::|::: | | :| |::: | | : :
 Db 167 VPGSTSGLTDNMSFVQRLKNWLLYLMNDMMFSHFMLSEWD----EYYSKVLGRRTTICEI 222

 Qy 241 LLKAELWFINSDFAFDFARPLLNPVYVGGLMKPIKVPQDLENFIAKFGDSGFVLVTL 300
 : ||::| | | : |::| | || | || | ||::|::| | : | : | : ||
 Db 223 MGKAEMWLIRSYWDFEFPRPFLPNFEYVGGHLCKPAKPLPEELEEFVQSSGNDGVVVFTL 282

 Qy 301 GSMVNTCQNPEIFKEMNN---AFAHLPGQVIWKCQCSHWPKDVHLAANVKIVDWLPQSD 356
 ||:: | | : :| :| | |::|::: | | | : : :|::|
 Db 283 GSMI---QN--LTEERSNLIASALAQIPQKVLWRYT---GKKPATLGPNTRLFEPQND 334

 Qy 357 LLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLK 416
 || || | |::|| | : || | ||||| ||::|::| | : | : :

Db 335 LLGHPKTRAFITHGGTNGLYEAIYHGVPMVGIPLEFGDQPDNIARVKAKGAAVDVLDRIMT 394

Qy 417 AETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVF 476
 :| :| :: : || |: | | || | | ||: |: : || ||:

Db 395 TSSLLKALKDVINNPSYKENAMKLSRIHHDQPLKPLDRAVFWIEFVMRHKGARHLRVAAH 454

Qy 477 QQPWHEQYLFDFVFLGLTLGLTLWLCCGK 505
 | : | || |||| :| |

Db 455 DLTWFQYYSLDVVFLTCVATIIFLAKK 483

RESULT 2

CGT_HUMAN

ID CGT_HUMAN STANDARD; PRT; 541 AA.

AC Q16880; O00196;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor

DE (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide

DE UDP-galactosyltransferase) (Cerebroside synthase).

GN UGT8 OR CGT OR UGT4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96299661; PubMed=8661025;

RA Bosio A., Binczek E., Lebeau M.M., Fernald A.A., Stoffel W.;

RT "The human gene CGT encoding the UDP-galactose ceramide galactosyl

RT transferase (cerebroside synthase): cloning, characterization, and

RT assignment to human chromosome 4, band q26.";

RL Genomics 34:69-75(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97242209; PubMed=9125199;

RA Kapitonov D.E., Yu R.K.;

RT "Cloning, characterization, and expression of human ceramide

RT galactosyltransferase cDNA.";

RL Biochem. Biophys. Res. Commun. 232:449-453(1997).

CC -!- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY

CC ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH

CC ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL

CC NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.

CC -!- CATALYTIC ACTIVITY: UDP-galactose + 2-(2-hydroxyacyl)sphingosine =

CC UDP + 1-(beta-D-galactosyl)-2-(2-hydroxyacyl)sphingosine.

CC -!- PATHWAY: Galactocerebroside biosynthesis.

CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.

CC -----

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CC -----
 DR EMBL; U30930; AAC50565.1; -.
 DR EMBL; U32370; AAC50815.1; -.
 DR EMBL; U31353; AAC50815.1; JOINED.
 DR EMBL; U31461; AAC50815.1; JOINED.
 DR EMBL; U31658; AAC50815.1; JOINED.
 DR EMBL; U31861; AAC50815.1; JOINED.
 DR EMBL; U62899; AAC51187.1; -.
 DR Genew; HGNC:12555; UGT8.
 DR MIM; 601291; -.
 DR GO; GO:0008489; F:UDP-galactose-glucosylceramide beta-1,4-gal. . .; TAS.
 DR GO; GO:0007417; P:central nervous system development; TAS.
 DR GO; GO:0007422; P:peripheral nervous system development; TAS.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Microsome.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 541 2-HYDROXYACYLSPHINGOSINE 1-BETA-
 FT GALACTOSYLTRANSFERASE.
 FT TRANSMEM 472 492 POTENTIAL.
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 99 99 T -> P (IN REF. 2).
 FT CONFLICT 116 116 L -> M (IN REF. 2).
 FT CONFLICT 356 356 L -> V (IN REF. 2).
 FT CONFLICT 379 379 L -> V (IN REF. 2).
 SQ SEQUENCE 541 AA; 61455 MW; EC532798F7E15834 CRC64;

Query Match 25.3%; Score 699; DB 1; Length 541;
 Best Local Similarity 32.2%; Pred. No. 2.9e-47;
 Matches 166; Conservative 95; Mismatches 185; Indels 70; Gaps 12;

Qy 13 LLPGVLLSEAAKIITISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70
 | | ::|||: : : || : :: | : ||: | :: |
 Db 11 LWSAVGIKAAKIIIVPPIMFESHMYIFKTLASALHERGHHTVFLLEGRD----- 61
 Qy 71 EKSYQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119
 :|| :| : : | ||: : || | :::
 Db 62 -----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAIELFDILDHYTK 112
 Qy 120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGLSLEFGLPI 179
 | : :: || | ||::|: | | :|| || : : : || |
 Db 113 NCDLMVGNHALIQLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172
 Qy 180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQHM-----QSTFD 222
 ||:||| | |||| | : | :|| ||: : | | : : |
 Db 173 PLAYVPEFNSLLTDRMNLQRMKNTGVYLISRLGVSVFLVLPKYERIMQKYNLLPEKSMYD 232
 Qy 223 NTIKEHFTGSRPVLSHLLLKAEWLFINSDFAFDFAFARPLLNTVYVGGIMEKPIKVPVQD 282
 | : : || : : | : | || || | ||| : : || | : : |
 Db 233 -----LVHGSSLWMLCTDVALEFPRLPLPNVYVGGILTKPASPLPED 275
 Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCShwPKDVHL 342
 | : : : ||||: | : | : : | : || ||| : || : |

Db	276	LQRWVNGANEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFs---- <td>331</td>	331
Qy	343	AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQOPENMVRVE	402
Db	332	GNNTKLI EWLPQNDLLGHSKIKAFLSHGGLNSIFETMYHGVPPVVGIPLFQGDHYDTMTRVQ	391
Qy	403	AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGVWDHV	462
Db	392	AKGMGILLEWKTVTEKELYEALVKVINNPYSYRQRAQKLSEIHKDQPGHPVNRTIYWIDYI	451
Qy	463	LQTGGATHLKPYPVFPQWPHEQYLFQDV-FVLLGLTL	497
Db	452	IRHNGAHLRAAVHQISFCQYFLLDIAFVLLLGAAL	487

RESULT 3

CGT MOUSE

```

ID      CGT_MOUSE      STANDARD;      PRT;      541 AA.
AC      Q64676; Q61634;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor
DE      (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide
DE      UDP-galactosyltransferase) (Cerebroside synthase).
GN      UGT8 OR CGT OR UGT4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Bosio A., Binczek E., Stoffel W.;
RL      Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Coetzee T., Li X., Fujita N., Marcus J., Suzuki K., Francke U.,
RA      Popko B.;
RL      Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY
CC      ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH
CC      ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL
CC      NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.
CC      -!- CATALYTIC ACTIVITY: UDP-galactose + 2-(2-hydroxyacyl)sphingosine =
CC      UDP + 1-(beta-D-galactosyl)-2-(2-hydroxyacyl)sphingosine.
CC      -!- PATHWAY: Galactocerebroside biosynthesis.
CC      -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC      -----
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DR EMBL; X92122; CAA63090.1; -.
 DR EMBL; X92123; CAA63091.1; -.
 DR EMBL; X92124; CAA63091.1; JOINED.
 DR EMBL; X92125; CAA63091.1; JOINED.
 DR EMBL; X92126; CAA63091.1; JOINED.
 DR EMBL; X92177; CAA63091.1; JOINED.
 DR EMBL; U48896; AAC53576.1; -.
 DR EMBL; U48892; AAC53576.1; JOINED.
 DR EMBL; U48893; AAC53576.1; JOINED.
 DR EMBL; U48894; AAC53576.1; JOINED.
 DR MGD; MGI:109522; Ugt8.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Microsome.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 541 2-HYDROXYACYLSPHINGOSINE 1-BETA-
 FT GALACTOSYLTRANSFERASE.
 FT TRANSMEM 472 492 POTENTIAL.
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 335 335 T -> S (IN REF. 2).
 FT CONFLICT 458 458 H -> R (IN REF. 2).
 FT CONFLICT 511 511 K -> E (IN REF. 2).
 FT CONFLICT 524 524 P -> R (IN REF. 2).
 FT CONFLICT 533 534 HI -> RV (IN REF. 2).
 FT CONFLICT 541 541 K -> R (IN REF. 2).
 SQ SEQUENCE 541 AA; 61137 MW; B76F80A9B5326EE8 CRC64;

Query Match 25.2%; Score 697; DB 1; Length 541;
 Best Local Similarity 32.4%; Pred. No. 4.2e-47;
 Matches 167; Conservative 95; Mismatches 184; Indels 70; Gaps 12;

Qy 13 LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70
 | | :: ||| : : : | | : :: | : ||: | :| : |
 Db 11 LWSAVGIARAAKIIIVPPIMFESHLYIFKTLASALHERGHHTVLLLEGRD----- 61
 Qy 71 EKSQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119
 :|| :| : : | | ||: : || |::|::
 Db 62 -----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAVELVDILDHYTK 112
 Qy 120 QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPI 179
 | : : :: || | ||::|: | | |:: || : : : | | |
 Db 113 NCDMMVGNQALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172
 Qy 180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCCRQOH----MQSTFD 222
 ||:||| | |||| | :| | :|| ||: : | | :| :|
 Db 173 PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRIGVSFLVLPKYERIMQKYNLLPAKSMYD 232
 Qy 223 NTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLEPNTVYVGGIMEKPIKVPVQD 282
 | : : || : :| | :| || ||| ||||:: || |::|
 Db 233 -----LVHGSSLWMLCTDVALEFPRTLPNVVYVGGILTTPASPLPED 275
 Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCSHWPKDVHL 342
 | : :: : ||||| : | : :| :: | ||| ||| : : | :|

Db	276	LQRWVSGAQEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---KPKNL	331
Qy	343	AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVE	402
		: : : : : : : :	
Db	332	GNNTKLI EWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVFVVGIPLFGDHYDTMTRVQ	391
Qy	403	AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV	462
		: : : : : : : : : : : :	
Db	392	AKGMGILLEWNTVTGELYDALVKVINNPYSYRQRAQKLSEIHKDQPGHPVNRTTYWIDYI	451
Qy	463	LQTGGATHLKPYPVFQQPWHEQYLFQDV-FVFLGLTL	497
		: : : : : :	
Db	452	LRHDGAHHLRSVAVHOISFCQYFLLDIAFVLLLGAVL	487

RESULT 4

CGT RAT

```

ID      CGT_RAT          STANDARD;      PRT;      541 AA.
AC      Q09426;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor
DE      (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide
DE      UDP-galactosyltransferase) (Cerebroside synthase).
GN      UGT8 OR CGT OR UGT4.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar; TISSUE=Brain;
RX      MEDLINE=94052143; PubMed=7694285;
RA      Schulte S., Stoffel W.;
RT      "Ceramide UDPgalactosyltransferase from myelinating rat brain:
RT      purification, cloning, and expression.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:10265-10269(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Brain;
RX      MEDLINE=94358923; PubMed=7521399;
RA      Stahl N., Jurevics H., Morell P., Suzuki K., Popko B.;
RT      "Isolation, characterization, and expression of cDNA clones that
RT      encode rat UDP-galactose: ceramide galactosyltransferase.";
RL      J. Neurosci. Res. 38:234-242(1994).
CC      -!- FUNCTION: CATALYZES THE TRANSFER OF GALACTOSE TO CERAMIDE, A KEY
CC      ENZYMATIC STEP IN THE BIOSYNTHESIS OF GALACTOCEREBROSIDES, WHICH
CC      ARE ABUNDANT SPHINGOLIPIDS OF THE MYELIN MEMBRANE OF THE CENTRAL
CC      NERVOUS SYSTEM AND PERIPHERAL NERVOUS SYSTEM.
CC      -!- CATALYTIC ACTIVITY: UDP-galactose + 2-(2-hydroxyacyl)sphingosine =
CC      UDP + 1-(beta-D-galactosyl)-2-(2-hydroxyacyl)sphingosine.
CC      -!- PATHWAY: Galactocerebroside biosynthesis.
CC      -!- TISSUE SPECIFICITY: BRAIN, RESTRICTED TO THE OLIGODENDROCYTE-
CC      CONTAINING CELL LAYERS OF CEREBRUM AND CEREBELLUM.
CC      -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC      -----

```

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 CC -----

DR EMBL; L21698; AAA16108.1; -.
 DR EMBL; U07683; AAA50212.1; -.
 DR PIR; A48801; A48801.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Microsome.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 541 2-HYDROXYACYLSPHINGOSINE 1-BETA-
 FT GALACTOSYLTRANSFERASE.
 FT TRANSMEM 472 492 POTENTIAL.
 FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 541 AA; 61126 MW; 260D7603170151BB CRC64;

Query Match 24.7%; Score 684; DB 1; Length 541;
 Best Local Similarity 32.2%; Pred. No. 4.4e-46;
 Matches 165; Conservative 94; Mismatches 184; Indels 70; Gaps 12;

Qy 13 LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70
 | | :: |||: : : || : :: | : ||: | :|: |
 Db 11 LWSAVGIARAAKIIIVPPIMFESHLYIFKTLASALHERGHHTVFLLEGRD----- 61
 Qy 71 EKSQYVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119
 : | :| : : | | ||: : || |::|::
 Db 62 -----IDPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAVELVDILDHYTK 112
 Qy 120 QCSHFLENRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLFGLPI 179
 | : : :: || | ||::|: | | |::| | : : : | | |
 Db 113 NCDMMVGNQALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172
 Qy 180 PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH-----MQSTFD 222
 ||:||| | |||||:| |::| ||: : | | :|:|
 Db 173 PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRMGVSFVLVLPKYERIMQKYNLLPAKSMYD 232
 Qy 223 NTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPIKVPVQD 282
 |: : || : :| | :| || || | |||:: || |::|
 Db 233 -----LVHGSSLWMLCTDVALEFPRPTLPNVVYVGGILTTPASPLPED 275
 Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShwPKDVHL 342
 |: :: : |||||: | : | : :| : || |||: : | :|
 Db 276 LQRWVDGAQEHEGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---KPKNL 331
 Qy 343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVVGIPFGDQPENMVRVE 402
 | |::| |||: || | :|| |::|| | | : |||: ||||| : | ||:
 Db 332 GNNTKLI EWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVVVGIPFGDHYDTMTRVQ 391

Qy 403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
 || | : : : : | : : : : | : | | : | | | : || : :
 Db 392 AKGMGILLEWNTVTEGELYDALVKVINNPSYRQRAQKLSEIHKDQPGHPVNRTTYWIDYI 451
 Qy 463 LQTGGATHLKPYVFQQPWHEQYLFDV-FVFLLG 494
 | : || || : | | : : : | : || |||
 Db 452 LRHDGAHHLRSVHQISFCQYFLLDIAFVLLLG 484

RESULT 5

UD11_HUMAN

ID UD11_HUMAN STANDARD; PRT; 533 AA.
 AC P22309;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE UDP-glucuronosyltransferase 1-1 precursor, microsomal (EC 2.4.1.17)
 DE (UDP-glucuronosyltransferase 1A1) (UDPGT) (UGT1*1) (UGT1-01) (UGT1.1)
 DE (UGT-1A) (UGT1A) (Bilirubin specific UDPGT isozyme 1) (HUG-BR1).
 GN UGT1A1 OR UGT1 OR GNT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91093210; PubMed=1898728;
 RA Ritter J.K., Crawford J.M., Owens I.S.;
 RT "Cloning of two human liver bilirubin UDP-glucuronosyltransferase
 RT cDNAs with expression in COS-1 cells."
 RL J. Biol. Chem. 266:1043-1047(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=92147680; PubMed=1339448;
 RA Ritter J.K., Chen F., Sheen Y.Y., Tran H.M., Kimura S., Yeatman M.T.,
 RA Owens I.S.;
 RT "A novel complex locus UGT1 encodes human bilirubin, phenol, and
 RT other UDP-glucuronosyltransferase isozymes with identical carboxyl
 RT termini."
 RL J. Biol. Chem. 267:3257-3261(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21327373; PubMed=11434514;
 RA Gong Q.H., Cho J.W., Huang T., Potter C., Gholami N., Basu N.K.,
 RA Kubota S., Carvalho S., Pennington M.W., Owens I.S., Popescu N.C.;
 RT "Thirteen UDP-glucuronosyltransferase genes are encoded at the human
 RT UGT1 gene complex locus."
 RL Pharmacogenetics 11:357-368(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Gattung S., Stoneking T., Davidson T.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE OF 1-50 FROM N.A.
 RA Ueyama H., Koiwai O., Soeda Y., Sato H., Satoh Y., Ohkubo I.,
 RA Doida Y.;

RT "Analysis of the promoter of human bilirubin
 RT UDP-glucuronosyltransferase gene (UGT1*1) in relevance to Gilbert's
 RT syndrome.";
 RL Hepatol. Res. 9:152-163(1997).
 RN [6]
 RP VARIANT CN-I PHE-375.
 RX MEDLINE=92339803; PubMed=1634050;
 RA Bosma P.J., Chowdhury J.R., Huang T.-J., Lahiri P., Elferink R.P.J.O.,
 RA van Es H.H.G., Lederstein M., Whittington P.F., Jansen P.L.M.,
 RA Chowdhury N.R.;
 RT "Mechanisms of inherited deficiencies of multiple UDP-
 RT glucuronosyltransferase isoforms in two patients with Crigler-Najjar
 RT syndrome, type I.";
 RL FASEB J. 6:2859-2863(1992).
 RN [7]
 RP VARIANTS CN-II ARG-71 AND ASP-486.
 RX MEDLINE=94107323; PubMed=8280139;
 RA Aono S., Yamada Y., Keino H., Hanada N., Nakagawa T., Sasaoka Y.,
 RA Yazawa T., Sato H., Koiwai O.;
 RT "Identification of defect in the genes for bilirubin UDP-glucuronosyl-
 RT transferase in a patient with Crigler-Najjar syndrome type II.";
 RL Biochem. Biophys. Res. Commun. 197:1239-1244(1993).
 RN [8]
 RP VARIANT CN-II ARG-331.
 RX MEDLINE=94102756; PubMed=8276413;
 RA Moghrabi N., Clarke D.J., Boxer M., Burchell B.;
 RT "Identification of an A-to-G missense mutation in exon 2 of the UGT1
 RT gene complex that causes Crigler-Najjar syndrome type 2.";
 RL Genomics 18:171-173(1993).
 RN [9]
 RP VARIANT CN-I PHE-170 DEL.
 RX MEDLINE=94043159; PubMed=8226884;
 RA Ritter J.K., Yeatman M.T., Kaiser C., Gridelli B., Owens I.S.;
 RT "A phenylalanine codon deletion at the UGT1 gene complex locus of a
 RT Crigler-Najjar type I patient generates a pH-sensitive bilirubin UDP-
 RT glucuronosyltransferase.";
 RL J. Biol. Chem. 268:23573-23579(1993).
 RN [10]
 RP VARIANTS CN-I VAL-292; GLU-308; ARG-357; THR-368; ARG-381; PRO-401 AND
 RP GLU-428.
 RX MEDLINE=95080780; PubMed=7989045;
 RA Labrune P., Myara A., Hadchouel M., Ronchi F., Bernard O., Trivin F.,
 RA Roy Chowdhury N., Roy Chowdhury J., Munnich A., Odievre M.;
 RT "Genetic heterogeneity of Crigler-Najjar syndrome type I: a study of
 RT 14 cases.";
 RL Hum. Genet. 94:693-697(1994).
 RN [11]
 RP VARIANTS CN GLU-175; ARG-177; TRP-209; ARG-276 AND PHE-375.
 RX MEDLINE=95081424; PubMed=7989595;
 RA Seppen J., Bosma P.J., Goldhoorn B.G., Bakker C.T.M.,
 RA Roy Chowdhury J., Roy Chowdhury N., Jansen P.L.M.,
 RA Oude Elferink R.P.J.;
 RT "Discrimination between Crigler-Najjar type I and II by expression of
 RT mutant bilirubin uridine diphosphate-glucuronosyltransferase.";
 RL J. Clin. Invest. 94:2385-2391(1994).
 RN [12]
 RP VARIANTS GILBERT SYNDROME ARG-71; GLN-229 AND GLY-367.

RC TISSUE=Liver, and Peripheral blood leukocytes;
 RX MEDLINE=95231122; PubMed=7715297;
 RA Aono S., Adachi Y., Uyama E., Yamada Y., Keino H., Nanno T.,
 RA Koiwai O., Sato H.;
 RT "Analysis of genes for bilirubin UDP-glucuronosyltransferase in
 RT Gilbert's syndrome.";
 RL Lancet 345:958-959(1995).
 RN [13]
 RP VARIANTS CN II ARG-71; TRP-209; GLN-229 AND ASP-486.
 RX MEDLINE=98284535; PubMed=9621515;
 RA Yamamoto K., Soeda Y., Kamisako T., Hosaka H., Fukano M., Sato H.,
 RA Fujiyama Y., Dachi Y., Satoh Y., Bamba T.;
 RT "Analysis of bilirubin uridine 5'-diphosphate (UDP)-
 RT glucuronosyltransferase gene mutations in seven patients with Crigler-
 RT Najjar syndrome type II.";
 RL J. Hum. Genet. 43:111-114(1998).
 RN [14]
 RP VARIANT GILBERT SYNDROME ASP-486.
 RX MEDLINE=98291073; PubMed=9627603;
 RA Maruo Y., Sato H., Yamano T., Doida Y., Shimada M.;
 RT "Gilbert syndrome caused by a homozygous missense mutation (Tyr486Asp)
 RT of bilirubin UDP-glucuronosyltransferase gene.";
 RL J. Pediatr. 132:1045-1047(1998).
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and
 CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds. This isoform glucuronidates bilirubin IX-
 CC alpha to form both the IX-alpha-C8 and IX-alpha-C12 monoconjugates
 CC and diconjugate.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced. The different
 CC isozymes have a different N-terminal domain and a common
 CC C-terminal domain of 245 residues;
 CC Name=1;
 CC IsoId=P22309-1; Sequence=Displayed;
 CC -!- TISSUE SPECIFICITY: Expressed in liver. Not expressed in skin or
 CC kidney.
 CC -!- DISEASE: THE GILBERT'S SYNDROME IS SHOWN TO OCCUR AS A CONSEQUENCE
 CC OF REDUCED BILIRUBIN TRANSFERASE ACTIVITY. THE DISORDER, IS MOST
 CC OFTEN DETECTED IN YOUNG ADULTS WITH VAGUE NONSPECIFIC COMPLAINTS.
 CC A MORE SEVERE INHERITABLE DEFICIENCY IN BILIRUBIN ACTIVITY EXIST
 CC IN CRIGLER-NAJJAR (CN): PATIENTS WITH TYPE I (RECESSIVE TRAIT)
 CC HAVE SEVERE HYPERBILIRUBINEMIA AND USUALLY DIE OF KERNICTERUS
 CC (BILIRUBIN ACCUMULATION IN THE BASAL GANGLIA AND BRAINSTEM NUCLEI)
 CC WITHIN THE FIRST YEAR OF LIFE. PATIENTS WITH TYPE II (DOMINANT
 CC TRAIT) HAVE LESS SEVERE HYPERBILIRUBINEMIA AND USUALLY SURVIVE
 CC INTO ADULTHOOD WITHOUT NEUROLOGIC DAMAGE. PHENOBARBITAL, WHICH
 CC INDUCES THE PARTIALLY DEFICIENT GLUCURONYL TRANSFERASE, CAN
 CC DIMINISH THE JAUNDICE.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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DR EMBL; M84125; AAA61248.1; -.
DR EMBL; M84124; AAA61247.1; ALT_SEQ.
DR EMBL; M84122; AAA61247.1; JOINED.
DR EMBL; M84123; AAA61247.1; JOINED.
DR EMBL; M57899; AAA63195.1; -.
DR EMBL; AF297093; AAG30424.1; -.
DR EMBL; AC006985; AAF03522.1; -.
DR EMBL; D87674; BAA25600.1; -.
DR PIR; A39092; A39092.
DR Genew; HGNC:12530; UGT1A1.
DR MIM; 191740; -.
DR MIM; 143500; -.
DR MIM; 218800; -.
DR MIM; 606785; -.
DR GO; GO:0006789; P:bilirubin conjugation; TAS.
DR GO; GO:0008210; P:estrogen metabolism; TAS.
DR InterPro; IPR002213; UDP_gluco_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
KW Multigene family; Microsome; Alternative splicing; Disease mutation.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 533 UDP-GLUCURONOSYLTRANSFERASE 1-1.
FT TRANSMEM 491 507 POTENTIAL.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 71 71 G -> R (IN CRIGLER-NAJJAR TYPE II AND
FT GILBERT SYNDROME).
FT /FTid=VAR_009504.
FT VARIANT 170 170 MISSING (IN CRIGLER-NAJJAR TYPE I; HAS
FT NEARLY NORMAL ACTIVITY AT PH 7.6 AND IS
FT INACTIVE AT PH 6.4).
FT /FTid=VAR_007695.
FT VARIANT 175 175 L -> E (IN CRIGLER-NAJJAR TYPE II).

Query Match 24.5%; Score 679; DB 1; Length 533;
Best Local Similarity 33.8%; Pred. No. 1.1e-45;
Matches 175; Conservative 93; Mismatches 211; Indels 38; Gaps 13;

Qy 8 LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHNKRGPFMP 65
|::| || |::| ||| | | ||:| | | | | : :| |
Db 11 LVLGLLLCVLGPVVS HAGKILLI-PVDGSHWLSMLGAIQQIQRGHEIVVL-----AP 62

Qy 66 D---FKKEEKSYQVISWLAPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL 111
| : :: | : :: | || | : || | ||: : : :
Db 63 DASLYIRDGAFYTLKTY--PVPFQREDVKESFVSLGHNVFENDSFLQRVI---KTYKKIK 117

Qy 112 NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFG 171
| ||| | : |::| || : ||:: : | | : | : | | | |
Db 118 KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC 177

Qy 172 SLEF---GLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCCRQOHMQSTFDNTIKEH 228
 |||| | | |||| | :|| | |||| |: || : | : | :
 Db 178 SLEFEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE 236

Qy 229 FTEGSRPVLSHLLKLAELWFINSDFAFDFARPLLPNTVYVGGLMEKPIKVPQDLENFIA 288
 | : : || | :| || | : ||: || |: ||| : | : | : |
 Db 237 FLQ-REVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVFGGINCLHQNPLSQEFAYIN 295

Qy 289 KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKI 348
 | : | | : ||||| : : : | : || | : | : : || | :
 Db 296 ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLANNITIL 351

Qy 349 VDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPFLFGDQPENMVRVEAKKFGV 408
 | ||||: || | | : || | : : | : | : |||| : ||||| : | | : | ||
 Db 352 VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFGDQMDNAKRMETKGAGV 411

Qy 409 SIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA 468
 : : : : | | : | : || || : | : : | : | | : | : : ||
 Db 412 TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKA 471

Qy 469 THLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWLCGK 505
 ||: | | : : || || | : | : : |
 Db 472 PHLRPAADLTWYQYHSLDVIGFLLAVLTVAFITFK 508

RESULT 6

UDB2_RAT

ID UDB2_RAT STANDARD; PRT; 530 AA.
 AC P08541;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE UDP-glucuronosyltransferase 2B2 precursor, microsomal (EC 2.4.1.17)
 DE (UDPGT) (3-hydroxyandrogen specific) (UDPGTR-4) (RLUG23).
 GN UGT2B2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=87033594; PubMed=2429951;
 RA McKenzie P.I.;
 RT "Rat liver UDP-glucuronosyltransferase. cDNA sequence and expression
 RT of a form glucuronidating 3-hydroxyandrogens.";
 RL J. Biol. Chem. 261:14112-14117(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91369480; PubMed=1909872;
 RA Haque S.J., Peterson D.D., Nebert D.W., McKenzie P.I.;
 RT "Isolation, sequence, and developmental expression of rat UGT2B2: the
 RT gene encoding a constitutive UDP glucuronosyltransferase that
 RT metabolizes etiocholanolone and androsterone.";
 RL DNA Cell Biol. 10:515-524(1991).
 RN [3]
 RP SEQUENCE OF 30-530 FROM N.A.

RC TISSUE=Liver;
 RX MEDLINE=86120371; PubMed=3003696;
 RA Jackson M.R.; Burchell B.;
 RT "The full length coding sequence of rat liver androsterone UDP-
 RT glucuronyltransferase cDNA and comparison with other members of this
 RT gene family.";
 RL Nucleic Acids Res. 14:779-795(1986).
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS. 2B2 ACTS ON VARIOUS ENDOGENOUS STEROIDS,
 CC ESPECIALLY ETIOCHOLANOLONE AND ANDROSTERONE.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- INDUCTION: Constitutively expressed.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; J02589; AAA42314.1; -.
 DR EMBL; M74439; -; NOT_ANNOTATED_CDS.
 DR EMBL; X03478; CAA27198.1; -.
 DR PIR; A40467; A40467.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B2.
 FT TRANSMEM 494 510 POTENTIAL.
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 159 159 D -> E (IN REF. 3).
 FT CONFLICT 286 286 A -> S (IN REF. 3).
 FT CONFLICT 351 351 N -> I (IN REF. 3).
 FT CONFLICT 363 363 L -> I (IN REF. 3).
 SQ SEQUENCE 530 AA; 60985MW; F2FFF3E23E2D75B2 CRC64;

Query Match 24.5%; Score 677.5; DB 1; Length 530;
 Best Local Similarity 33.5%; Pred. No. 1.4e-45;
 Matches 170; Conservative 87; Mismatches 218; Indels 33; Gaps 13;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISW-LAPEDHQREFKKS 92
 ||::: : | ||||: | : :: | :::: | ||
 Db 34 SHWMNIKIILDELVQRGHEVTVLKPSAYFFLDPKKSSDLKFEIFSTSISKDELQNHFIKL 93
 Qy 93 FDFFL--TLGGRGKFENLLNVLEYLALQ-CSHFLNRKDIMDSLKNENFDMVIVET 146
 | : | | :||: | | | :| :| | : ||:: :
 Db 94 LDVWTYELPRDTCLSYSPILQNLVYEFSYFYLSICKDAVSNNKQLMTKLQESKFDVLFADP 153
 Qy 147 FDYCPFLIAEKLKGPVAILSTSFG-SLEFGLP---IPLSYVPVFRSLTDMDFWGRVK 202

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      | | | | | | : | | | | | : | | | | | | | | |
Db    154 VASCGDLIAELLHIPFLYSLSFSPGHKLEKSIGKFILPPSYVPVILSGLAGKMTFIDRVK 213

Qy    203 NF--LMFFSF-CRRQQHMQ-STFDNTIKEHFTEGSRPVLSHLLLKAEWFINSDFAFDFA 258
      | : : | | | : | : | | : | | : | | : |
Db    214 NMICMLYFDFWFERLRHKEWDTFYSEIL-----GRPTTVDETMASKVEIWLIRSYWDLKFP 268

Qy    259 RPLLENTVYVGGLMKEPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPFIKEMNN 318
      | | | | | : | | | | | : | : | : | : | : | : | : |
Db    269 HPTLPNVDIYIGGLHCKPAKPLPKDMEEFVQSSGEHGVVVFSLGSMVS-----NMTEEKAN 323

Qy    319 ----AFAHLPOGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLfvTHGGQNS 374
      | | : | | | : | | | | | | | : : | | | : | | | | |
Db    324 AIAWALAQIPQKVLWKFD---GKTPATLGPNTRVYKWLQNDLLGHPKTKAFVTHGGANG 380

Qy    375 IMEAIQHGVMVGIPPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK 434
      : | | | | : | | : | | | | | : | : | | : : : : : : |
Db    381 LYEAIIYHGIPMIGIPLFGDQPDNIAHMAVAKGAASLNIRTMSKLDFLSALEEVIDNPFYK 440

Qy    435 SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLLG 494
      : | | | | : | | | | | : : : | | | : | | : : | | |
Db    441 KNVMLLSTIHHDQPMKPLDRAVFWIEFIMRHKGAKHLRPLGHNLPWYQYHSLDVIGFLLT 500

Qy    495 LTLGTLWLCGK-LLGMAVWWLRGARKVK 521
      | | | | | : : : : | : |
Db    501 CFAVIAALTVMKCLLEMYRFFVKKEKKMK 528

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RESULT 7

UDBK_MACFA

```

ID    UDBK_MACFA      STANDARD;      PRT;    530 AA.
AC    077649;
DT    15-DEC-1998 (Rel. 37, Created)
DT    15-DEC-1998 (Rel. 37, Last sequence update)
DT    28-FEB-2003 (Rel. 41, Last annotation update)
DE    UDP-glucuronosyltransferase 2B20 precursor, microsomal (EC 2.4.1.17)
DE    (UDPGT).
GN    UGT2B20.
OS    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC    Cercopithecinae; Macaca.
OX    NCBI_TaxID=9541;
RN    [1]
RP    SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC    TISSUE=Liver, and Prostate;
RX    MEDLINE=99112924; PubMed=9895303;
RA    Barbier O., Belanger A., Hum D.W.;
RT    "Cloning and characterization of a simian UDP-glucuronosyltransferase
RT    enzyme UGT2B20, a novel C19 steroid-conjugating protein.";
RL    Biochem. J. 337:567-574(1999).
CC    -!- FUNCTION: UDPGTs are of major importance in the conjugation and
CC    subsequent elimination of potentially toxic xenobiotics and
CC    endogenous compounds. This isozyme has glucuronidating capacity
CC    with androgens, such as testosterone, dihydrotestosterone (DHT)
CC    and 3alpha-Diol. It is also active on catecholoeestrogens including
CC    1,3,5,10-oestratriene-3, 4-diol-17-one.

```

CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; AF072223; AAD08808.1; -.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 530 UDP-GLUCURONOSYLTRANSFERASE 2B20.
 FT TRANSMEM 495 515 POTENTIAL.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 530 AA; 61225 MW; A5EB47F8D517D8DA CRC64;

Query Match 24.3%; Score 673; DB 1; Length 530;
 Best Local Similarity 32.9%; Pred. No. 3.1e-45;
 Matches 160; Conservative 85; Mismatches 218; Indels 24; Gaps 10;

Qy 34 SHYLLMDRVSQILQDHGHNVMTLNHKGPFMPDFKKEEKSYQVI-SWLAPEDHQREFKKS 92
 ||:: | : : | | |:: | : | : : | : |
 Db 34 SHWINMKTILEELVRRRHEVTVLTSASTFVNDKSSAIKFEVYPTSLTRKNDMEDSLMKL 93
 Qy 93 FDFLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMVIV 144
 | : | : : | : | : | : | : | : | : :
 Db 94 LDIWTYSI--SNSTFLSYFSKLQELCWEYYYSEKLCKDAVLNKKLMTKLKETKFDVILA 151
 Qy 145 ETFDYCPFLIAEKLKGPVFAVILSTSFG-SLE---FGLPIPLSYVPVFRSLTLDHMDFWGR 200
 : : | |:: | | | | : : | : | | | | | | : : | |
 Db 152 DALNPCGELLAELFNIPFVYSLRFTVGYTFEKNGGGFLFPSPYVPVVMSELSDQMTFTTER 211
 Qy 201 VKNFL--MFFSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHLLLKAEWFINSDFAFDFA 258
 : | : : : | | | : | | : | : | : | : | : : | :
 Db 212 IKNMIHKLYFDFW-FQIHDIKKWDQFYSE--VLGRPTTLFETMRKAEMWLIPTYWDFEFP 268
 Qy 259 RPLLNTVYVGGIMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPFIKEMNN 318
 | | | | : | | | | | | : : : | : : | : : | : : : :
 Db 269 RPFLPNVDFVGGHLHCKPAKPLPKEMEETFVQSSGENGVVVFSLGSMISN-MSEERANMIAS 327
 Qy 319 AFAHLPPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEA 378
 | | : | | : | : | : : | : : | : : | : : | : : | :
 Db 328 ALAQIPQKVLWKFD---GKKPNTLGSNTRYKWLFPQNDLLGHPKTKAFITHGGTNGIYEA 384
 Qy 379 IQHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAV 438

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      | ||:||||||| || :|:| :: |   :|: :: : : |   :| :: : || |:
Db      385 IYHGIPMVGIPLFADQHDNIVHMKVGAALSVDIRTMSSRDLLNALKSVINEPIYKENAM 444

Qy      439 AASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLGLGLTLG 498
      | |   |: | | | ||: |:: || ||:   | : : || |||
Db      445 KLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWQYHSLDVIAFLACVAA 504

Qy      499 TLWLCGK 505
      ::: |
Db      505 VIFIITK 511

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RESULT 8

UDBD_RABIT

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ID      UDBD_RABIT      STANDARD;      PRT;      531 AA.
AC      P36512;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      UDP-glucuronosyltransferase 2B13 precursor, microsomal (EC 2.4.1.17)
DE      (UDPGT) (EGT10).
GN      UGT2B13.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=New Zealand white; TISSUE=Liver;
RX      MEDLINE=93315511; PubMed=8325897;
RA      Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
RT      "Cloning and characterization of rabbit liver UDP-
RT      glucuronosyltransferase cDNAs. Developmental and inducible expression
RT      of 4-hydroxybiphenyl UGT2B13.";
RL      J. Biol. Chem. 268:15260-15266(1993).
CC      -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC      SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC      ENDOGENOUS COMPOUNDS. ACTS ON SMALL PHENOLIC AGENTS SUCH AS 2-
CC      NAPHTOL AND 4-METHYLBELLIFERONE AS WELL AS BULKY PHENOLIC
CC      COMPOUNDS LIKE 2-HYDROXY- AND 4-HYDROXYBIPHENYL. IN CONTRAST TO
CC      2B16 IT IS ACTIVE TOWARD OCTYLGALLATE.
CC      -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
CC      beta-D-glucuronoside.
CC      -!- SUBCELLULAR LOCATION: Microsomal.
CC      -!- DEVELOPMENTAL STAGE: Expressed primarily in adult rabbits.
CC      -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
DR      EMBL; L01081; AAA18020.1; -.
DR      PIR; B47113; B47113.

```

DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome.
 FT SIGNAL 1 24
 FT CHAIN 25 531 UDP-GLUCURONOSYLTRANSFERASE 2B13.
 FT TRANSMEM 495 511 POTENTIAL.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 531 AA; 60552 MW; 961DA58AC4CB9932 CRC64;

Query Match 24.2%; Score 670; DB 1; Length 531;
 .Best Local Similarity 32.6%; Pred. No. 5.4e-45;
 Matches 169; Conservative 90; Mismatches 206; Indels 54; Gaps 14;

```

Qy      34 SHYLLMDRVSQILQDHGHNVMTL-----NHKRG----PFMPDFKKEEKSYQVISW 79
      ||:: | : | || ||:| |:: | | ::::| : |
Db      35 SHWMNMKTILDALVQQGHEVTVLRSSASIVIGSNNESGIKFETFHTSYRKDEIENFFMDW 94

Qy      80 LAPEDHQREFKKSFDFFLE---ETLGGRGKFENLLNVLEYLAL---QCSHFLNRKDIMDS 133
      :| :: :| || :::| : | : | :|
Db      95 F-----YKMIYNVSIESYWETFS-----LTKMVILKYSDICEDICKEVILNKKLMTK 141

Qy     134 LKNENFDMVIVETFDYCPFLIAEKLKGP-----FVAILSTSFGSLEFGLPIPLSYVPV 186
      |: ||:: : :||| | | || : | ||| | |||
Db     142 LQESRFDVVLADPVSPGGELLAELLKIPLVYSLRGFVGYMLQKHGG---GLLLPPSYVPV 198

Qy     187 FRSLTDMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHFTEGSRPV--LSHLLLK 243
      | | | ||:| | :| | : : :| | || | :|
Db     199 MMSGGLGSQMTFMERVQNLLCVLYFDFW--FPKFNEKRWDQFYSEVL---GRPVTFLELMGK 254

Qy     244 AELWFINSDFAFDFARPLLENTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSM 303
      |:| | | : :| ||||| :||| || ||:|:|:|:| :| | | :|||
Db     255 ADMWLIRSYWDLEFPRPLLPNDFIGGLHCKPAKPLPQEMEDFVQSSGEEGVVVFSLGSM 314

Qy     304 VNTCQNPEIFKEMNNAFAHLPQGVWKCQCShWPKDVHLAANVKIVDWLPQSDLLAHPSI 363
      :: | : :| | || |:: : | | :| :: |:|:| ||
Db     315 ISNL-TEERANVIASALAQLPQKVLWRFE---GKKPDMLGSNTRLYKWIPQNDLLGHPKT 370

Qy     364 RLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAETLALK 423
      : |:| || | : || ||:| ||:| ||||| :|:| :|| | : || : : |
Db     371 KAFITHGGANGVFEAIYHGIPMVGLPLFGDQLDNIVYMKAKGAAVKLNLTMTSSADLLNA 430

Qy     424 MKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQ 483
      :| :: | || | : | | | :| | | ||:|:| || ||: |::
Db     431 LKTVINDPSYKENAMTSLRIHHDQPMKPLDRAVFWIEYVMRHKGAKHLRVAHDLTWYQY 490

Qy     484 YLFDVFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKE 522
      : || || | :| | : : || | | :
Db     491 HSLDVIGFLLACVAITTYLIVKCCLLVYRYVLGAGKKKK 529

```

RESULT 9

UD11_MOUSE

ID UD11_MOUSE STANDARD; PRT; 535 AA.

AC Q63886;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE UDP-glucuronosyltransferase 1-1 precursor, microsomal (EC 2.4.1.17)
 DE (UDPGT) (UGT1*1) (UGT1-01) (UGT1.1) (UGT1A1) (UGTBR1).
 GN UGT1A1 OR UGT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93219265; PubMed=8464825;
 RA Kong A.N., Ma M., Tao D., Yang L.;
 RT "Molecular cloning of two cDNAs encoding the mouse bilirubin/phenol
 RT family of UDP-glucuronosyltransferases (mUGTBr/p).";
 RL Pharm. Res. 10:461-465(1993).
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and
 CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced. The different
 CC isozymes have a different N-terminal domain and a common
 CC C-terminal domain of 245 residues;
 CC Name=1;
 CC IsoId=Q63886-1; Sequence=Displayed;
 CC -!- INDUCTION: By dioxin.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; S64760; AAB26033.2; -.
 DR MGD; MGI:98898; Ugt1a1.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome; Alternative splicing.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 535 UDP-GLUCURONOSYLTRANSFERASE 1-1.
 FT TRANSMEM 493 509 POTENTIAL.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 535 AA; 60123 MW; B5AE3C209979BBB8 CRC64;

Query Match 24.2%; Score 669; DB 1; Length 535;
Best Local Similarity 31.7%; Pred. No. 6.6e-45;
Matches 174; Conservative 101; Mismatches 216; Indels 58; Gaps 15;

```
5 RVL LLVG FLLP ---GVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 61
|:|:|: :| | | :| : : | | :| | | | | :| :|
9 RLLLLLPYLLLCVFGPYASHAGRL -VFPMDGSHWLSMLGVIQQLQKKGHEVVVI ---A 63

y 62 PFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFEN ---LLNVLE-YL 117
| | | : : | | :| :| | | | | :| :| :|
b 64 PEASIHKEGSEFYTLRKFVPVFQ ---KENV TATIVEL --GRTAFNQDSFLLRVVKIYM 116

Qy 118 ALQ ---CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGP ---FVAI 165
:| :| :| :| :| :| :| :| :| :| :| :|
Db 117 KVKRDSMLLAGCSHLLHNAEFMASLEESHFDALLTDPFLPCGSIVAQYLTVPTVYFLNK 176

Qy 166 LSTSFSGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFS ---FCRRQQHMQSTFD 222
| | | :| | | | | :| :| :| | | :| :| :|
Db 177 LPCSLDSEATQCPVPLSYVPKSLSENSDRMNF LQRVKNVLLAVSENEMCRVVYSPYGS LA 236

Qy 223 NTIKEHFTEGSRPVLSHLLKAE LWFINSDFAFDFARPLLNTVYVGLMEKPIKVPVQD 282
| : :| :| :| :| :| :| :| :| :| :| :| :|
Db 237 TEILQ ---KEVTQD LLSPASIWLMRSDFKDYPRPIMPNMVFIGGINCLQKKPLSQE 291

Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHL PQGVIWKCQC SHWPKDVHL 342
| :| :| :| :| :| :| :| :| :| :| :| :|
Db 292 FEAYVNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTVLWRYTGT ---RPSNL 347

Qy 343 AANVKIVDWLPQSDLLAHP SIRLFVTHGGQNSIMEAIQHGVPMVGIPLEFGDQ PENMVRVE 402
| | :| :| :| :| :| :| :| :| :| :| :| :|
Db 348 AKNTILVKWL PQNDLIGHPKTRAFITHSGSHGIYEGICNGVPMVMMLPFGDQMDNAKRME 407

Qy 403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
:| :| :| :| :| :| :| :| :| :| :| :| :|
Db 408 TRGAGVT LNVLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAVFWVEYV 467

Qy 463 LQTGGATHLKPYVVFQQPWHEQYLFDFVFLGLTLGLTLWL ---CGKLLGMVAVWWL 514
:| :| :| :| :| :| :| :| :| :| :| :|
Db 468 MRHKGAPHLRPA AHDLTWYQYHSLDVIGFLLAIVLT VVFVIFVKCCAYGCRKCFG --- 521

Qy 515 RGARKVKET 523
| :| :| :|
Db 522 -GKGRVKKS 529
```

RESULT 10

UDB1_RAT

ID UDB1_RAT STANDARD; PRT; 529 AA.

AC P09875;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE UDP-glucuronosyltransferase 2B1 precursor, microsomal (EC 2.4.1.17)

DE (UDPGT) (UDPGTR-2).

GN UGT2B1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86196018; PubMed=3084479;
 RA McKenzie P.I.;
 RT "Rat liver UDP-glucuronosyltransferase. Sequence and expression of a
 RT cDNA encoding a phenobarbital-inducible form.";
 RL J. Biol. Chem. 261:6119-6125(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90293083; PubMed=2113533;
 RA McKenzie P.I., Rodbourn L.;
 RT "Organization of the rat UDP-glucuronosyltransferase, UDPGTr-2, gene
 RT and characterization of its promoter.";
 RL J. Biol. Chem. 265:11328-11332(1990).
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and
 CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- INDUCTION: By phenobarbital.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; M13506; AAA42313.1; -.
 DR EMBL; M35086; AAA42310.1; -.
 DR EMBL; M35202; AAA42310.1; JOINED.
 DR EMBL; M35080; AAA42310.1; JOINED.
 DR EMBL; M35082; AAA42310.1; JOINED.
 DR EMBL; M35083; AAA42310.1; JOINED.
 DR PIR; A42233; A42233.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 529 UDP-GLUCURONOSYLTRANSFERASE 2B1.
 FT TRANSMEM 494 510 POTENTIAL.
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 529 AA; 60484 MW; 14DF0224BF1C3044 CRC64;

Query Match 24.1%; Score 668; DB 1; Length 529;
 Best Local Similarity 32.2%; Pred. No. 7.8e-45;
 Matches 175; Conservative 89; Mismatches 229; Indels 50; Gaps 15;

Qy 6 VLLLVGFLLPGLVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
 Db 11 LIQLICYFRPGA----CGKVLVWPT-EYSHWINIKIILNELAQRGHEVTVLVSSASILIE 65

Qy 66 DFKKEEKSYQVISW-LAPEDHQREFKKSDFDFLE--ETLG---GRGKFENLLN---VLE 115
 Db 66 PTKESSINFEIYSVPLSKSDLEYSFAKWIDEWTRDFETLSIWTTYYSKMVKVFNEYSADVVE 125

Qy 116 YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFAILSTSFG---- 171
 Db 126 NL---CKALIWNKSLMKKLQGSQFDVILADAVGPCGELLAELLKTPLVYSLRFCPGYRCE 182

Qy 172 SLEFGLPIPLSYVPVFRSLTLDHMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHF 229
 Db 183 KFSGGLPLPPSYVPVVLSELSDRMTFVERVKNMLQMLYFDF-----WFQPFKEKSWSQFY 237

Qy 230 TE--GSRPVLSHLLLKAEWLFINSDFAFDFARLLPNTVYVGGIMEKPIKPVPQDLENFI 287
 Db 238 SDVLGRPTTLTEMMGKADIWLIRTFWDLEFPHPLPNFDFVGGHLHCKPAKPLPREMEEFV 297

Qy 288 AKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCSHWPKDVHLAANVK 347
 Db 298 QSSGEHGVVVFSLGSMVKNL-TEEKANVVASALAQIPQKVWVRFD---GKKPDTLGSNTR 353

Qy 348 IVDWLPQSDLLAHPsirLfvthggqnsimeaiqhgvpmvgiplfGDQpenmvrveakkfg 407
 Db 354 LYKWIPQNDLLGHPKTKAFVAHGGTNGIYEAIYHGIPIVGIPLFADQPDNINHMVAKGAA 413

Qy 408 VSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGG 467
 Db 414 VRVDFSILSTTGLLTALKIVMNDPSYKENAMRLSRIHHDQPVKPLDRAVFWIEYVMRHKG 473

Qy 468 ATHLKPYVFQQPWHEQYLFDFVFLGLTLGT-----LWLCGKLLGMAVWWLRGARK 519
 Db 474 AKHLRSTLHDLSWFQYHSLDVIGFLLLCVGVVFIITKFCCLFCCRKTANM-----GKK 526

Qy 520 VKE 522
 Db 527 KKE 529

RESULT 11

UD15_RAT

ID UD15_RAT STANDARD; PRT; 531 AA.

AC Q64638;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE UDP-glucuronosyltransferase 1-5 precursor, microsomal (EC 2.4.1.17)

DE (UDPGT) (UGT1*5) (UGT1-05) (UGT1.5) (UGT1A5) (B5).

GN UGT1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE OF 1-286 FROM N.A.

RC STRAIN=Wistar;
 RX MEDLINE=95332265; PubMed=7608130;
 RA Emi Y., Ikushiro S.I., Iyanagi T.;
 RT "Drug-responsive and tissue-specific alternative expression of
 RT multiple first exons in rat UDP-glucuronosyltransferase family 1
 RT (UGT1) gene complex.";
 RL J. Biochem. 117:392-399(1995).
 RN [2]
 RP SEQUENCE OF 287-531 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90274676; PubMed=2112380;
 RA Sato H., Koiwai O., Tanabe K., Kashiwamata S.;
 RT "Isolation and sequencing of rat liver bilirubin UDP-
 RT glucuronosyltransferase cDNA: possible alternate splicing of a common
 RT primary transcript.";
 RL Biochem. Biophys. Res. Commun. 169:260-264(1990).
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and
 CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms may be produced. Isoforms have a
 CC different N-terminal domain and a common C-terminal domain of
 CC 245 residues;
 CC Name=1;
 CC IsoId=Q64638-1; Sequence=Displayed;
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D38069; BAA07263.1; -.
 DR EMBL; M34007; AAA42312.1; ALT_TERM.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome; Alternative splicing.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 531 UDP-GLUCURONOSYLTRANSFERASE 1-5.
 FT TRANSMEM 489 505 POTENTIAL.
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 531 AA; 59993 MW; 04148C1BA6CAAC80 CRC64;

Query Match

24.0%; Score 665; DB 1; Length 531;

Best Local Similarity 30.5%; Pred. No. 1.3e-44;
Matches 169; Conservative 102; Mismatches 216; Indels 68; Gaps 15;

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHHR 60
      : |   ||| : : |   : | : | : : ||| : | | : |   || : |
Db      7 LQGLAGLLLLLYALP---WAEKGKVL-VFPMEGSHWLSMRDVVRELHARGHQAVVL---- 58

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQ-----REFKKSFD-----FFLEETLGGRGKF 107
      | :   ||| : : : : |   |   |   | :   ||| :
Db     59 APEVTVHIKEEDFFTLLQTYVPVYTRQGFRQQMMRNIVVFETGNYVKTFLETS----- 111

Qy    108 ENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGP---FVA 164
      | | : |   | : | : : : | : ||| : :   | : | : || | | : |
Db    112 EILKNISTVLLRSCMNLLHNGSLLQHLNSSSFDMVLTDPVIPCGQVLAKYLGIPTVFFLR 171

Qy    165 ILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH 216
      :   |   | | ||| : : ||| |   ||| :   ||| | :
Db    172 YIPCGIDSEATQCPKPSSYIPNLLTMSDHMTFLQRVKNMLYPLALKYICHFSFTRYESL 231

Qy    217 MQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGGLMEKPI 276
      :   |   ||| |   : |   || ||| : || : ||| : ||| :
Db    232 ASELLQREVS--LVE---VLSH---ASVWLFRGDFVFDYPRPVMNPMVFIGGINCVIK 281

Qy    277 KPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIVKQCQSHW 336
      || : | : : : | : | : : ||| : :   | : |   : || : : : :
Db    282 KPLSQEFEAYVNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTLWRYTGT-- 338

Qy    337 PKDVHLAANVKIVDWLPQSDLLAHPsirLFTVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPE 396
      :   || | : | ||| : || | | : || | : | | : ||| | : ||| | :
Db    339 -RPSNLAKNTILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMPLFGDQMD 397

Qy    397 NMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLV 456
      | | : | : || : : : : | : | : : : | | : | : : | : | |
Db    398 NAKRMETRGAGVTNLNVLEMTADDLENALKTVINNKSYKENIMRLSSLHKDRPIEPLDLAV 457

Qy    457 GWIDHVLQTGGATHLKPYPVFQPPWHEQYLFDFVFLGLTLGLTLWL-----CGKLLG 508
      | : : | : : || ||| : | : : : || ||| : | : : :   | | |
Db    458 FWVEYVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG 517

Qy    509 MAVWWLRGARKVKET 523
      | : || :
Db    518 -----GKGRVKKS 525

```

RESULT 12

UDBJ_MACFA

ID UDBJ_MACFA STANDARD; PRT; 528 AA.

AC Q9XT55;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE UDP-glucuronosyltransferase 2B19 precursor, microsomal (EC 2.4.1.17).

GN UGT2B19.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.

OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Prostate;
 RX MEDLINE=99203465; PubMed=10102998;
 RA Belanger G., Barbier O., Hum D.W., Belanger A.;
 RT "Molecular cloning, expression and characterization of a monkey
 RT steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates
 RT testosterone.";
 RL Eur. J. Biochem. 260:701-708(1999).
 CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS. THIS ISOZYME DISPLAYS ACTIVITY TOWARD
 CC SEVERAL CLASSES OF XENOBIOTIC SUBSTRATES: EUGENOL, 4-
 CC METHYLLUMBELLIFERONE, P-NITROPHENOL, 1-NAPHTHOL, P,P'-BIPHENOL,
 CC NARINGENIN AND O,O'-BIPHENOL. ACTIVE ALSO ON 3A-HYDROXY AND 17B-
 CC HYDROXY POSITIONS OF STEROIDS.
 CC -!- FUNCTION: CONTRIBUTES TO THE FORMATION OF ANDROGEN GLUCURONIDE IN
 CC EXTRAHEPATIC STEROID TARGET TISSUES SUCH AS THE PROSTATE.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal (By similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, OVARY, PROSTATE, COLON,
 CC KIDNEY, PANCREAS, BRAIN, CEREBELLUM, MAMMARY GLAND AND EPIDIDYMIS.
 CC NOT EXPRESSED IN SMALL INTESTINE, SPLEEN, BLADDER, ADRENAL GLAND
 CC AND TESTIS.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; AF112112; AAD24435.1; -.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 528 UDP-GLUCURONOSYLTRANSFERASE 2B19.
 FT TRANSMEM 493 513 POTENTIAL.
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 528 AA; 60741 MW; 3BFD2AE714A27AEE CRC64;

Query Match 24.0%; Score 664.5; DB 1; Length 528;
 Best Local Similarity 33.2%; Pred. No. 1.5e-44;
 Matches 168; Conservative 89; Mismatches 218; Indels 31; Gaps 12;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRG-----PFMPDFKKEEKSYQVISWLAPEDHQREF 89
 ||:: : : | ||||: : | | | : : :| :
 Db 34 SHWMNIKTILDELVQRGHEVTVLAYSTSILPDPNPNPSPLKFEICPTSLTETEFQDSVTQL 93
 Qy 90 KKSFDFFLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMV 142

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      | :   ::|   : : | : | :   |   : : | : | :   ||:|
Db      94 VKRWSDIRKDTF-----WPHFLHVQEMMWTYGDMIRKFCKDVVSNNKKLMKKLQESRFDVV 148

Qy      143 IVETFDYCPFLIAEKLKGPFVAILSTSFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFW 198
      : :   | | : || |   || |   | | : ||   |   | |||| | | | | |
Db      149 LADAISPCGELLAELLKIPFVYSLRFS PGYALEKHGGGFLFPFSYVPVTMSELRDQMTFM 208

Qy      199 GRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFD 256
      ||:|   ::::| | :   :: : |   :   |   | : : |||:| | : : |
Db      209 ERVQNMIYMVYFDFWFQVWDVKN-WDQFYSK--VLGRPTTLFEIMAKAEIWLIRNYWDFQ 265

Qy      257 FARPLLNTVYVGGLMKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEM 316
      |   |||| | : || | || ||: : : | | :   ||:| | : : |||||:   : | :
Db      266 FPHPLLPNVEFVGGLHCKPAKPLPKEMEETFVQSSGDNGVVVFSLGSMVSN-MSEERANVI 324

Qy      317 NNAFAHLPPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFTVTHGGQNSIM 376
      : | | : || | : | :   :   |   |   | : :   ||||: || | | | : |||| | |
Db      325 ASALAKIPQKVLWRFDGN---KPD TLGLNTQLYKWLPQNDLLGH PKTRAFITHGGANGIY 381

Qy      377 EAIQHGVPMVGIP LF GDQ PENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
      ||| ||: ||||: ||| |||: | :   : : |   : | : : | | |
Db      382 EAIYHGIPMVGVP LFADQPDNIAHMKAKGAAVRLDFDTMSSTDLLNALKTVINDPIYKEN 441

Qy      437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFELLGLT 496
      | : | |   | : | | | ||: | : : || ||:   | : : || |||
Db      442 AMKLSSIHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHDLTWFQYHSLDVIGFLLACV 501

Qy      497 LGTLWLCGKLLGMAVW-WLRGARKVK 521
      : : : | |   || : : | : | |
Db      502 ATVIFIITKCL-FCVWKFVRTRKKGK 526

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RESULT 13

UDB9_MACFA

```

ID      UDB9_MACFA      STANDARD;      PRT;      529 AA.
AC      002663;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      UDP-glucuronosyltransferase 2B9 precursor, microsomal (EC 2.4.1.17)
DE      (UDPGT).
GN      UGT2B9.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Prostate;
RX      MEDLINE=98030212; PubMed=9364930;
RA      Belanger G., Beaulieu M., Levesque E., Hum D.W., Belanger A.;
RT      "Expression and characterization of a novel
RT      UDP-glucuronosyltransferase, UGT2B9, from cynomolgus monkey.";
RL      DNA Cell Biol. 16:1195-1205(1997).
CC      -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC      SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

```

CC ENDOGENOUS COMPOUNDS. THIS ISOZYME IS ACTIVE ON C18, C19, AND C21
 CC STEROIDS, BILE ACIDS, AND SEVERAL XENOBIOTICS INCLUDING EUGENOL,
 CC 1-NAPHTHOL, AND P-NITROPHENOL.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; U91582; AAB50249.1; -.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Bile acid catabolism; Transferase; Glycosyltransferase; Microsome;
 KW Signal; Transmembrane; Glycoprotein; Multigene family.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 529 UDP-GLUCURONOSYLTRANSFERASE 2B9.
 FT TRANSMEM 494 514 POTENTIAL.
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 529 AA; 60970 MW; F110F85FE3A9DB8D CRC64;

Query Match 24.0%; Score 663.5; DB 1; Length 529;
 Best Local Similarity 32.9%; Pred. No. 1.8e-44;
 Matches 169; Conservative 78; Mismatches 220; Indels 47; Gaps 13;

Qy 34 SHYLLMDRVSQILQDHGHNVTML-----NH----KRGPFMPDFKKEE----KSYQ 75
 ||:: | : : | || ||:| : | | | :
 Db 34 SHWMNMKTILEELVQRGHEVTVLASSASILFDPNNSSALKIEVFPTSLTKTEFENISMQE 93
 Qy 76 VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSL 134
 | |: |:| :| : : :| :: | :: | :|
 Db 94 VKRWIELPKD-----TFWLYFSQMQEIMWRFGDIIRNF-----CKDVVSNKKLMKKL 140
 Qy 135 KNENFDMVIVETFDYCPFLIAEKLGPFPVAILSTSFGSLEF-----GLPIPLSYVPVFRS 189
 : ||:| : | :|| | | : | : | | |||| |
 Db 141 QESRFDVVFADPIFPCSELLAELFNIPLVYSLRFTPGYI-FEKHCGGFLFPSPSYVPVMS 199
 Qy 190 LLTDHMDFWGRVKNFLMFFSF-CRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF 248
 |:| | | ||| : || : :| | | || : ||::|
 Db 200 ELSDQMTFMERVKNMIYMLSFDYFQMYDMKKWDQFYSE--VLGRPTTLSETMGKADIWL 257
 Qy 249 INSDFAFDFARPLLPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQ 308
 | : : | | |||| :||| || ||:|:::| |: |:| |: :||| |
 Db 258 IRNSWNFQFPHPLLPNVDFVGLHCKPAKPLPKEMEETFQSSGENGVVVFSLGSMV-TNM 316
 Qy 309 NPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVT 368
 | : : | :|| |:| : | | :| :||:| | | | :|
 Db 317 EEERANVIASALAQIPQKVLWRFD--GKKPDTLGLNTRLYKWIPQNDLLGHPKTRAFIT 373

QY 369 HGGQNSIMEAIQHGVPMVGIPFLGDPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIM 428
 ||| | | ||| ||||| |||:|: :: | | : : : || ::| ::
 Db 374 HGGANGIYEAIYHGVPMVGIPFLFADQPDNIAHMKTKGAAVRLDFDTMSSTDLANRLKTVI 433
 QY 429 EDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDV 488
 | || : | | |: | | ||: |: || ||:| | : : ||
 Db 434 NDPLYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLREAAHDLTWFFQYHSLDV 493
 QY 489 FVFLGLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
 ||| :: | | : ||| |:
 Db 494 IGFLACVATVIFVIMKCCFLFCFW--KFARKGKK 525

RESULT 14

UDBE_RABIT

ID UDBE_RABIT STANDARD; PRT; 530 AA.
 AC P36513;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE UDP-glucuronosyltransferase 2B14 precursor, microsomal (EC 2.4.1.17)
 DE (UDPGT) (EGT12).
 GN UGT2B14.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Liver;
 RX MEDLINE=93315511; PubMed=8325897;
 RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
 RT "Cloning and characterization of rabbit liver UDP-
 RT glucuronosyltransferase cDNAs. Developmental and inducible expression
 RT of 4-hydroxybiphenyl UGT2B13.";
 RL J. Biol. Chem. 268:15260-15266(1993).
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and
 CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- DEVELOPMENTAL STAGE: Expressed primarily in adult rabbits.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC -----
 DR EMBL; L01082; AAA18021.1; -.
 DR PIR; C47113; C47113.
 DR InterPro; IPR002213; UDP_gluco_trans.

GN UGT2B4 OR UGT2B11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=87241362; PubMed=3109396;
 RA Jackson M.R., McCarthy L.R., Harding D., Wilson S., Coughtrie M.W.H.,
 RA Burchell B.;
 RT "Cloning of a human liver microsomal UDP-glucuronosyltransferase
 RT cDNA.";
 RL Biochem. J. 242:581-588(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93326164; PubMed=8333863;
 RA Jin C.-J., Miners J.O., Lillywhite K.J., McKenzie P.I.;
 RT "cDNA cloning and expression of two new members of the human liver
 RT UDP-glucuronosyltransferase 2B subfamily.";
 RL Biochem. Biophys. Res. Commun. 194:496-503(1993).
 RN [3]
 RP SEQUENCE FROM N.A., VARIANT GLU-458, AND CHARACTERIZATION.
 RX MEDLINE=99303261; PubMed=10376768;
 RA Levesque E., Beaulieu M., Hum D.W., Belanger A.;
 RT "Characterization and substrate specificity of UGT2B4 (E458): a
 RT UDP-glucuronosyltransferase encoded by a polymorphic gene.";
 RL Pharmacogenetics 9:207-216(1999).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS LEU-109 AND LEU-396.
 RA McKenzie P.I.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Riedy M., Miller A.;
 RT "Genomic organization and structure of the UGT2B gene complex at human
 RT chromosome 4q13.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uzdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: UDPGTs are of major importance in the conjugation and
 CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds. This isozyme is active on polyhydroxylated
 CC estrogens (such as estriol, 4-hydroxyestrone and 2-hydroxyestriol)
 CC and xenobiotics (such as 4-methylumbelliferone, 1-naphthol, 4-
 CC nitrophenol, 2-aminophenol, 4-hydroxybiphenyl and menthol). It is
 CC capable of 6 alpha-hydroxyglucuronidation of hyodeoxycholic acid.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -!- CAUTION: REF.2 THOUGHT THAT THIS WAS A NEW FORM (UGT2B11). THE
 CC NAME UGT2B11 HAS NOW BEEN REUSED FOR ANOTHER HUMAN ENZYME.
 CC -----
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 CC -----
 DR EMBL; Y00317; CAA68415.1; -.
 DR EMBL; AF064200; AAC95002.1; -.
 DR EMBL; AJ005162; CAA06396.1; -.
 DR EMBL; AF081793; AAC32272.1; -.
 DR EMBL; AF135416; AAF78145.1; -.
 DR EMBL; BC026264; AAH26264.1; -.
 DR PIR; JN0619; JN0619.
 DR Genew; HGNC:12553; UGT2B4.
 DR MIM; 600067; -.
 DR GO; GO:0005792; C:microsome; NAS.
 DR GO; GO:0006711; P:estrogen catabolism; IDA.
 DR GO; GO:0006805; P:xenobiotic metabolism; IDA.
 DR InterPro; IPR002213; UDP_gluco_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
 KW Multigene family; Microsome; Polymorphism.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 528 UDP-GLUCURONOSYLTRANSFERASE 2B4.
 FT TRANSMEM 493 509 POTENTIAL.
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 109 109 F -> L.
 FT /FTid=VAR_011328.
 FT VARIANT 396 396 F -> L.
 FT /FTid=VAR_011329.
 FT VARIANT 458 458 D -> E.
 FT /FTid=VAR_007712.
 FT CONFLICT 171 172 SL -> RP (IN REF. 1).
 FT CONFLICT 291 293 EME -> KWK (IN REF. 4).

FT CONFLICT 382 387 EAIYHG -> KAISPR (IN REF. 1).
SQ SEQUENCE 528 AA; 60512 MW; 6B45E6769971A078 CRC64;

Query Match 23.9%; Score 661.5; DB 1; Length 528;
Best Local Similarity 34.2%; Pred. No. 2.5e-44;
Matches 173; Conservative 87; Mismatches 215; Indels 31; Gaps 15;

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Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRG----PFMPDFKKEEKSQVISWLAPEDHQREF 89
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Db      34 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSTLKFVYPVSLTKTEFEDIKQL 93

Qy      90 KKSFDFFLEETLGGRGKFENLLNVL----EYLALQCSHFLNRKDIMDSLKNENFDMVIVE 145
      | : ::| | : :: : | | :: | :| | : ||:: :
Db      94 VKRWAE LPKDTFW--SYFSQVQEIMWTFNDILRKFCCKDIVSNKKLMKKLQESRFDVVLAD 151

Qy     146 TFDYCPF--LIAEKLGPVFVAILSTSEFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWG 199
      || |::| | || | | | :| || | |||| | |::| |
Db     152 A--VFPFGELLAELLKIPFVYSLRSPGYAIEKHSGGLLFPPSYVPVVMSELSDQMTFIE 209

Qy     200 RVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDF 257
      |||| ::::| | : | : :| | | | : ||::| | : : | |
Db     210 RVKNMIYVLYFEFWFQIFDMKK-WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 266

Qy     258 ARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM 316
      |||| :||| || ||:|::| | : |::| | : :||| || : | :
Db     267 PHPLLPNVEFVGGLHCKPAKPLPKEMEEFVQSSGENGVVVFSLGSMVSNTSE--ERANVI 324

Qy     317 NNAFAHL PQGVIWKCQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIM 376
      :| | :|| |:: : | | | : : |::||| || | |::|| | |
Db     325 ASALAKIPQKVLWRFDGN---KPD TLGLNTRLYKWIPQNDLLGHPKTRAFITHGGANGIY 381

Qy     377 EAIQHGVPMVGIPLFQDPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
      ||| ||:||||:||| ||:| : ::|| ||: : : | :| :: | ||
Db     382 EAIYHGIPMVGVP LFADQPDNIAHMKAKGA AVSLDFHTMSSTDLLNALKTVINDPLYKEN 441

Qy     437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLT 496
      | : | | | : | | ||: |:: || ||: | : : || |||
Db     442 AMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA AHDLTWFQYHSLDVTGFLACV 501

Qy     497 LGTLWL CGKLLGMAVW-WLRGARKVK 521
      :: : | | || :| :| |
Db     502 ATVIFIITKCL-FCVWKFVRTGKKGK 526
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